

WEST Search History

DATE: Monday, June 21, 2004

Hide?	Set Name	Query	Hit Count
		<i>DB=USPT; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L18	L17 not l3	0
<input type="checkbox"/>	L17	L16 same l2	2
<input type="checkbox"/>	L16	catalytic adj domain	2478
<input type="checkbox"/>	L15	L14 not l3	2
<input type="checkbox"/>	L14	l2 same l13	4
<input type="checkbox"/>	L13	(c adj terminal) or (c-terminal) or (c adj terminus) or (c-terminus) or carboxyterminal or (carboxy adj terminal) or carboxyterminus or (carboxy adj terminus)	29825
<input type="checkbox"/>	L12	L2 same l7	3
<input type="checkbox"/>	L11	L2 near40 l7	0
<input type="checkbox"/>	L10	l2 near30 l7	0
<input type="checkbox"/>	L9	l2 and l7	52
<input type="checkbox"/>	L8	l2 near20 L7	0
<input type="checkbox"/>	L7	(fusion or fused) adj (protein or peptide)	18128
<input type="checkbox"/>	L6	L5 not l3	7
<input type="checkbox"/>	L5	l2 and L4	10
<input type="checkbox"/>	L4	james.in.	203604
<input type="checkbox"/>	L3	l1 and L2	3
<input type="checkbox"/>	L2	starch adj (synthase or synthetase)	197
<input type="checkbox"/>	L1	myers.in.	5098

END OF SEARCH HISTORY

Hit List

Clear	Generate Collection	Print	Fwd Refs	Blkwd Refs
Generate OACS				

Search Results - Record(s) 1 through 3 of 3 returned.

☐ 1. Document ID: US 6639125 B1

L3: Entry 1 of 3

File: USPT

Oct 28, 2003

US-PAT-NO: 6639125

DOCUMENT-IDENTIFIER: US 6639125 B1

TITLE: Dull1 coding for a starch synthase and uses thereof

Full	Title	Citation	Front	Review	Classification	Date	Reference	Abstract	Claims	Drawings	Other
------	-------	----------	-------	--------	----------------	------	-----------	----------	--------	----------	-------

☐ 2. Document ID: US 6410716 B1

L3: Entry 2 of 3

File: USPT

Jun 25, 2002

US-PAT-NO: 6410716

DOCUMENT-IDENTIFIER: US 6410716 B1

TITLE: Isolation of SU1, a starch debranching enzyme, the product of the maize gene sugary1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Abstract	Claims	Drawings	Other
------	-------	----------	-------	--------	----------------	------	-----------	----------	--------	----------	-------

☐ 3. Document ID: US 5981728 A

L3: Entry 3 of 3

File: USPT

Nov 9, 1999

US-PAT-NO: 5981728

DOCUMENT-IDENTIFIER: US 5981728 A

TITLE: Dull1 coding for a novel starch synthase and uses thereof

Full	Title	Citation	Front	Review	Classification	Date	Reference	Abstract	Claims	Drawings	Other
------	-------	----------	-------	--------	----------------	------	-----------	----------	--------	----------	-------

Clear	Generate Collection	Print	Fwd Refs	Blkwd Refs
Generate OACS				

Hit List

Clear	Generate Collection	Print	Fwd Refs	Bkwd Refs
Generate OACS				

Search Results - Record(s) 1 through 7 of 7 returned.

☐ 1. Document ID: US 6391551 B1

L6: Entry 1 of 7

File: USPT

May 21, 2002

US-PAT-NO: 6391551

DOCUMENT-IDENTIFIER: US 6391551 B1

TITLE: Detection of nucleic acid hybrids

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	Keywords	Drawings
------	-------	----------	-------	--------	----------------	------	-----------	--------	----------	----------

☐ 2. Document ID: US 6350934 B1

L6: Entry 2 of 7

File: USPT

Feb 26, 2002

US-PAT-NO: 6350934

DOCUMENT-IDENTIFIER: US 6350934 B1

TITLE: Nucleic acid encoding delta-9 desaturase

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	Keywords	Drawings
------	-------	----------	-------	--------	----------------	------	-----------	--------	----------	----------

☐ 3. Document ID: US 5675064 A

L6: Entry 3 of 7

File: USPT

Oct 7, 1997

US-PAT-NO: 5675064

DOCUMENT-IDENTIFIER: US 5675064 A

TITLE: Starch and grain with a novel genotype

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	Keywords	Drawings
------	-------	----------	-------	--------	----------------	------	-----------	--------	----------	----------

☐ 4. Document ID: US 5648249 A

L6: Entry 4 of 7

File: USPT

Jul 15, 1997

US-PAT-NO: 5648249

DOCUMENT-IDENTIFIER: US 5648249 A

TITLE: Method of improving the quality of stored potatoes

Full	Title	Citation	Front	Review	Classification	Date	Reference			Claims	RMK	Draw De
------	-------	----------	-------	--------	----------------	------	-----------	--	--	--------	-----	---------

☐ 5. Document ID: US 5648111 A

L6: Entry 5 of 7

File: USPT

Jul 15, 1997

US-PAT-NO: 5648111

DOCUMENT-IDENTIFIER: US 5648111 A

TITLE: Starch and grain with a novel genotype

Full	Title	Citation	Front	Review	Classification	Date	Reference			Claims	RMK	Draw De
------	-------	----------	-------	--------	----------------	------	-----------	--	--	--------	-----	---------

☐ 6. Document ID: US 5516939 A

L6: Entry 6 of 7

File: USPT

May 14, 1996

US-PAT-NO: 5516939

DOCUMENT-IDENTIFIER: US 5516939 A

TITLE: Starch and grain with a novel genotype

Full	Title	Citation	Front	Review	Classification	Date	Reference			Claims	RMK	Draw De
------	-------	----------	-------	--------	----------------	------	-----------	--	--	--------	-----	---------

☐ 7. Document ID: US 5502270 A

L6: Entry 7 of 7

File: USPT

Mar 26, 1996

US-PAT-NO: 5502270

DOCUMENT-IDENTIFIER: US 5502270 A

**** See image for Certificate of Correction ****

TITLE: Starch and grain with a novel genotype

Full	Title	Citation	Front	Review	Classification	Date	Reference			Claims	RMK	Draw De
------	-------	----------	-------	--------	----------------	------	-----------	--	--	--------	-----	---------

Clear

Generate Collection

Print

Fwd Refs

Bkwd Refs

Generate OACS

Terms

Documents

L5 not L3

7

Display Format:

TI

Change Format

[Previous Page](#)

[Next Page](#)

[Go to Doc#](#)

Hit List

Clear	Generate Collection	Print	Fwd Refs	Bkwd Refs
Generate OACS				

Search Results - Record(s) 1 through 3 of 3 returned.

☐ 1. Document ID: US 6642437 B1

L12: Entry 1 of 3

File: USPT

Nov 4, 2003

US-PAT-NO: 6642437

DOCUMENT-IDENTIFIER: US 6642437 B1

TITLE: Production of proteins in plant seeds

Full	Title	Citation	Front	Review	Classification	Date	Reference			Claims	RWC	Draw. De
------	-------	----------	-------	--------	----------------	------	-----------	--	--	--------	-----	----------

☐ 2. Document ID: US 6639125 B1

L12: Entry 2 of 3

File: USPT

Oct 28, 2003

US-PAT-NO: 6639125

DOCUMENT-IDENTIFIER: US 6639125 B1

TITLE: Dull1 coding for a starch synthase and uses thereof

Full	Title	Citation	Front	Review	Classification	Date	Reference			Claims	RWC	Draw. De
------	-------	----------	-------	--------	----------------	------	-----------	--	--	--------	-----	----------

☐ 3. Document ID: US 5981728 A

L12: Entry 3 of 3

File: USPT

Nov 9, 1999

US-PAT-NO: 5981728

DOCUMENT-IDENTIFIER: US 5981728 A

TITLE: Dull1 coding for a novel starch synthase and uses thereof

Full	Title	Citation	Front	Review	Classification	Date	Reference			Claims	RWC	Draw. De
------	-------	----------	-------	--------	----------------	------	-----------	--	--	--------	-----	----------

Clear	Generate Collection	Print	Fwd Refs	Bkwd Refs
Generate OACS				

Terms	Documents
-------	-----------

L2 same L7

3

Display Format:

TI

Change Format[Previous Page](#)[Next Page](#)[Go to Doc#](#)

Hit List

Clear	Generate Collection	Print	Fwd Refs	Bkwd Refs
Generate OACS				

Search Results - Record(s) 1 through 2 of 2 returned.

☐ 1. Document ID: US 6590141 B1

L15: Entry 1 of 2

File: USPT

Jul 8, 2003

US-PAT-NO: 6590141

DOCUMENT-IDENTIFIER: US 6590141 B1

TITLE: Nucleic acid molecules from plants encoding enzymes which participate in starch synthesis

Full	Title	Citation	Front	Review	Classification	Date	Reference	Suppl. Data	Pub. Info	Claims	RMK	Draw. Data
------	-------	----------	-------	--------	----------------	------	-----------	-------------	-----------	--------	-----	------------

☐ 2. Document ID: US 6476212 B1

L15: Entry 2 of 2

File: USPT

Nov 5, 2002

US-PAT-NO: 6476212

DOCUMENT-IDENTIFIER: US 6476212 B1

**** See image for Certificate of Correction ****

TITLE: Polynucleotides and polypeptides derived from corn ear

Full	Title	Citation	Front	Review	Classification	Date	Reference	Suppl. Data	Pub. Info	Claims	RMK	Draw. Data
------	-------	----------	-------	--------	----------------	------	-----------	-------------	-----------	--------	-----	------------

Clear	Generate Collection	Print	Fwd Refs	Bkwd Refs
Generate OACS				

Terms	Documents
L14 not L3	2

Display Format:

Change Format

[Previous Page](#)

[Next Page](#)

[Go to Doc#](#)

=> file ca

=> 's (starch(w) (synthase? or synthetase?))/ab,bi

L1 779 (STARCH(W) (SYNTHASE? OR SYNTHETASE?))/AB,BI

=> s (dull(w)1 or du1)/ab,bi

L2 36 (DULL(W)1 OR DU1)/AB,BI

=> s l1 or l2

L3 807 L1 OR L2

=> s (carboxyterminal or carboxyterminus or c(w)terminal or c(w)terminus or carb

L4 81907 (CARBOXYTERMINAL OR CARBOXYTERMINUS OR C(W)TERMINAL OR C(W)TERMI
NUS OR CARBOXY(W)TERMINAL OR CARBOXY(W)TERMINUS)/AB,BI

=> s l3(l)l4

L5 10 L3(L)L4

=> file biosis

=> s l5

L6 7 L3(L)L4

=> dup rem

L7 10 DUP REM L5 L6 (7 DUPLICATES REMOVED)

=> d l7 1-10 ti py

L7 ANSWER 1 OF 10 CA COPYRIGHT 2004 ACS on STN
TI Chimeric genes and starch synthases with heterologous glucan-binding and
glycosyltransferase domains and transgenic plants producing altered starch
PY 2002

L7 ANSWER 2 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 1
TI An immunoenzymatic solid-phase assay for quantitative determination of
HIV-1 protease activity
PY 2002

L7 ANSWER 3 OF 10 CA COPYRIGHT 2004 ACS on STN
TI Corn starch synthase isoenzyme and cDNA, transgenic plants expressing this
cDNA, and method for production of starches
PY 2001

L7 ANSWER 4 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 2
TI Chain-length specificities of maize starch synthase I enzyme: Studies of
glucan affinity and catalytic properties
PY 2001

L7 ANSWER 5 OF 10 CA COPYRIGHT 2004 ACS on STN
TI Fusion proteins with Chlamydomonas starch synthase and food and
pharmaceuticals containing starch-fusion protein complexes
PY 2000

L7 ANSWER 6 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 3
TI The structure and expression of the wheat starch synthase III gene. Motifs
in the expressed gene define the lineage of the starch synthase III gene
family
PY 2000

C7/5
Biosis
6/2/04

L7 ANSWER 7 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 4
 TI Expression of a cassava granule-bound starch synthase gene in the
 PY amylose-free potato only partially restores amylose content
 1999

L7 ANSWER 8 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 5
 TI Specificity of starch synthase isoforms from potato
 PY 1999

L7 ANSWER 9 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 6
 TI Identification of the soluble starch synthase activities of maize
 PY endosperm
 1999

L7 ANSWER 10 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 7
 TI Isolation and characterization of the zSSIa and zSSIb starch synthase
 PY cDNA clones from maize endosperm
 1998

=> d 17 ab 5-10

=> d 17 7 bib

L7 ANSWER 7 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 4
 AN 132:247052 CA
 TI Expression of a cassava granule-bound starch synthase gene in the
 AU amylose-free potato only partially restores amylose content
 Salehuzzaman, Shah N. I. M.; Vincken, Jean-Paul; Van De Wal, Marion;
 CS Straatman-Engelen, Irma; Jacobsen, Evert; Visser, Richard G. F.
 The Graduate School Experimental Plant Sciences, Laboratory of Plant
 SO Breeding, Wageningen Agricultural University, Wageningen, 6700 AJ, Neth.
 Plant, Cell and Environment (1999), 22(10), 1311-1318
 CODEN: PLCEDV; ISSN: 0140-7791
 PB Blackwell Science Ltd.
 DT Journal
 LA English

=> d 17 9 bib

L7 ANSWER 9 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 6
 AN 131:99886 CA
 TI Identification of the soluble starch synthase activities of maize
 AU endosperm
 Cao, Heping; Imparl-Radosevich, Jennifer; Guan, Hanping; Keeling, Peter
 L.; James, Martha G.; Myers, Alan M.
 CS Department of Biochemistry, Biophysics, and Molecular Biology, Iowa State
 University, Ames, IA, 50011, USA
 SO Plant Physiology (1999), 120(1), 205-215
 CODEN: PLPHAY; ISSN: 0032-0889
 PB American Society of Plant Physiologists
 DT Journal
 LA English

=> file ca

=> s (myers, a?)/au

L8 841 (MYERS, A?)/AU

=> s 11 and 18

L9 5 L1 AND L8

=> file biosis

=> s l9

L10 8 L1 AND L8

=> dup rem

L11 9 DUP REM L9 L10 (4 DUPLICATES REMOVED)

=> d l11 1-9

L11 ANSWER 1 OF 9 CA COPYRIGHT 2004 ACS on STN DUPLICATE 1

AN 139:334824 CA

TI Protein and cDNA sequences of corn gene dull1 coding for a ***starch***
synthase and use

IN ***Myers, Alan M.*** ; James, Martha Graham

PA Iowa State University Research Foundation, Inc., USA

SO U.S., 56 pp., Cont.-in-part of U.S. Ser. No. 968,542.

CODEN: USXXAM

DT Patent

LA English

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
	-----	----	-----	-----	-----
PI	US 6639125	B1	20031028	US 2000-554467	20000512
	US 5981728	A	19991109	US 1997-968542	19971112
	WO 9924575	A1	19990520	WO 1998-US24225	19981112

L11 ANSWER 2 OF 9 CA COPYRIGHT 2004 ACS on STN DUPLICATE 2

AN 132:133950 CA

TI Purification and characterization of soluble ***starch***
synthases from maize endosperm

AU Cao, Heping; James, Martha G.; ***Myers, Alan M.***

CS Department of Biochemistry, Biophysics, and Molecular Biology, Iowa State University, Ames, IA, 50011, USA

SO Archives of Biochemistry and Biophysics (2000), 373(1), 135-146

CODEN: ABBIA4; ISSN: 0003-9861

PB Academic Press

DT Journal

LA English

L11 ANSWER 3 OF 9 CA COPYRIGHT 2004 ACS on STN

AN 130:333760 CA

TI Maize ***starch*** ***synthase*** gene dul and uses in starch
production

IN ***Myers, Alan M.*** ; James, Martha G.

PA Iowa State University Research Foundation, Inc., USA

SO PCT Int. Appl., 138 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
	-----	----	-----	-----	-----
PI	WO 9924575	A1	19990520	WO 1998-US24225	19981112
	US 5981728	A	19991109	US 1997-968542	19971112
	CA 2309346	AA	19990520	CA 1998-2309346	19981112
	AU 9915236	A1	19990531	AU 1999-15236	19981112
	AU 761419	B2	20030605		
	EP 1030922	A1	20000830	EP 1998-959440	19981112
	BR 9814864	A	20011106	BR 1998-14864	19981112
	JP 2001522604	T2	20011120	JP 2000-520569	19981112
	NZ 504534	A	20021220	NZ 1998-504534	19981112
	MX 200004586	A	20001110	MX 2000-4586	20000512
	US 6639125	B1	20031028	US 2000-554467	20000512

L11 ANSWER 4 OF 9 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 2000:278998 BIOSIS
 DN PREV200000278998
 TI Dull1 coding for a novel ***starch*** ***synthase*** and uses
 thereof.
 AU ***Myers, Alan M.*** [Inventor, Reprint author]; James, Martha G.
 [Inventor]
 CS Des Moines, IA, USA
 ASSIGNEE: Iowa State University Research Foundation, Inc., Ames, IA, USA
 PI US 5981728 November 09, 1999

L11 ANSWER 5 OF 9 CA COPYRIGHT 2004 ACS on STN DUPLICATE 3
 AN 131:99886 CA
 TI Identification of the soluble ***starch*** ***synthase***
 activities of maize endosperm
 AU Cao, Heping; Imparl-Radosevich, Jennifer; Guan, Hanping; Keeling, Peter
 L.; James, Martha G.; ***Myers, Alan M.***
 CS Department of Biochemistry, Biophysics, and Molecular Biology, Iowa State
 University, Ames, IA, 50011, USA
 SO Plant Physiology (1999), 120(1), 205-215
 CODEN: PLPHAY; ISSN: 0032-0889
 PB American Society of Plant Physiologists
 DT Journal
 LA English

L11 ANSWER 6 OF 9 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 2003:144471 BIOSIS
 DN PREV200300144471
 TI Identification and characterization of the ***starch***
 synthase activity coded for by maize gene dull1.
 AU Cao, Heping [Reprint Author]; ***Myers, Alan M.*** ; James, Martha G.
 CS Department of Biochemistry, Biophysics, and Molecular Biology, Iowa State
 University, Ames, IA, USA
 hpcao@iastate.edu
 SO Plant Biology (Rockville), (1999) Vol. 1999, pp. 193. print.
 Meeting Info.: Annual Meeting of the American Society of Plant
 Physiologists. Baltimore, Maryland, USA. July 24-28, 1999. American
 Society of Plant Physiologists (ASPP).
 DT Conference; (Meeting)
 Conference; (Meeting Poster)
 Conference; Abstract; (Meeting Abstract)
 LA English

L11 ANSWER 7 OF 9 CA COPYRIGHT 2004 ACS on STN DUPLICATE 4
 AN 129:2125 CA
 TI Characterization of dull1, a maize gene coding for a novel ***starch***
 synthase
 AU Gao, Ming; Wanat, Jennifer; Stinard, Philip S.; James, Martha G.;
 Myers, Alan M.
 CS Department of Biochemistry and Biophysics, Iowa State University, Ames,
 IA, 50011, USA
 SO Plant Cell (1998), 10(3), 399-412
 CODEN: PLCEEW; ISSN: 1040-4651
 PB American Society of Plant Physiologists
 DT Journal
 LA English

L11 ANSWER 8 OF 9 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 2003:119968 BIOSIS
 DN PREV200300119968
 TI Identification of DU1 protein as a major soluble ***starch***

. ***synthase*** in maize kernels.
AU Cao, Heping [Reprint Author]; James, Martha G. [Reprint Author];
 Myers, Alan M. [Reprint Author]
CS Iowa State University, Ames, IA, USA
SO Plant Biology (Rockville), (1998) Vol. 1998, pp. 119. print.
 Meeting Info.: Annual Meeting of the American Society of Plant
 Physiologists combined with the 9th International Conference on
 Arabidopsis Research. Madison, WI, USA. June 27-July 01, 1998. American
 Society of Plant Physiologists (ASPP).
DT Conference; (Meeting)
 Conference; (Meeting Poster)
 Conference; Abstract; (Meeting Abstract)
LA English

L11 ANSWER 9 OF 9 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2003:89137 BIOSIS
DN PREV200300089137
TI Identification of DU1 protein as a major soluble ***starch***
 synthase in maize kernels.
AU Cao, Heping [Reprint Author]; Mou, Beiquan [Reprint Author]; James, Martha
 G. [Reprint Author]; ***Myers, Alan M.*** [Reprint Author]
CS Iowa State University, Ames, IA, USA
SO Plant Biology (Rockville), (1998) Vol. 1998, pp. 25. print.
 Meeting Info.: Annual Meeting of the American Society of Plant
 Physiologists combined with the 9th International Conference on
 Arabidopsis Research. Madison, WI, USA. June 27-July 01, 1998. American
 Society of Plant Physiologists (ASPP).
DT Conference; (Meeting)
 Conference; Abstract; (Meeting Abstract)
LA English

=> file ca

=> s (james, m?)/au
L12 1148 (JAMES, M?)/AU

=> s l12 and l1
L13 5 L12 AND L1

=> s l13 not l9
L14 0 L13 NOT L9

=> file biosis

=> s l14
L15 0 L13 NOT L9

=> log y
STN INTERNATIONAL LOGOFF AT 21:07:09 ON 21 JUN 2004

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 20, 2004, 03:45:55 ; Search time 16042 Seconds
(without alignments)
7019.399 Million cell updates/sec

Title: US-10-634-262-1_COPY_2425_5022

Perfect score: 2598

Sequence: 1 agctgtgtgaaaaaattat.....gctgaacaggcgatctcag 2598

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.on.*

21: em.or.*

22: em.ov.*

23: em.pat.*

24: em.ph.*

25: em.pl.*

26: em.ro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg.hum.*

31: em.htg.inv.*

32: em.htg.other.*

33: em.htg.mus.*

34: em.htg.pln.*

35: em.htg.rod.*

36: em.htg.man.*

37: em.htg.vrt.*

38: em.sv.*

39: em.htgo.hum.*

40: em.htgo.mus.*

41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2598	100.0	6027	6	AR085480	Sequence
2	2598	100.0	6027	6	AR427878	Sequence
3	2598	100.0	6027	6	BD091317	Dulli cod
4	2598	100.0	6027	8	AF023159	Zea mays
5	1766.6	68.0	5346	8	AF258608	Triticum
6	1703.8	65.6	5760	6	AX653280	Sequence
7	1647.2	63.4	4241	8	AX127098	Orzya sat
8	1646.8	63.4	3645	6	AX654187	Sequence
9	1581.4	60.9	3032	6	AX755430	Sequence
10	1500.4	57.8	4121	6	AR353090	Sequence
11	1500.4	57.8	4121	6	AX085557	Sequence
12	1217.6	46.9	3901	8	VUA225088	Vigna ung
13	1206.4	46.4	4127	6	A63216	Sequence 3
14	1206.4	46.4	4127	8	STSS	X95759 S.tuberosum
15	1204.8	46.4	4167	8	STSSIII	X94400 S.tuberosum
16	1204.8	46.4	4168	6	A51209	Sequence 11
17	1204.8	46.4	4168	6	AR112889	Sequence
18	1204.8	46.4	4168	6	AR256404	Sequence
19	1141.2	43.9	3078	6	AX651938	Sequence
20	931	35.8	2303	6	A51199	Sequence 1
21	931	35.8	2303	6	AR112884	Sequence
22	931	35.8	2303	6	AR256399	Sequence
23	739.4	28.5	1826	8	AK059368	Orzya sat
24	501	19.3	11550	8	AF258609	Regilops
25	485	18.7	138993	8	AP005441	Orzya sat
26	485	18.7	142044	2	AP004660	Orzya sat
27	483.4	18.6	9586	8	AX100469	Orzya sat
28	444.4	17.1	8821	8	AF432315	Orzya sat
29	444.4	17.1	187601	8	OSJN00079	Orzya sat
30	271.6	10.5	91566	8	F25C20	Arabidops
31	186.2	7.2	1856	6	AF023160	Zea mays
32	175	6.7	212	6	AR244742	Sequence
33	147.6	5.7	3519	8	VUN005752	Vigna ung
34	145	5.6	2652	6	A93857	Sequence 1
35	145	5.6	2652	6	AR145490	Sequence
36	145	5.6	2652	6	AR399209	Sequence
37	144.8	5.6	3434	6	AR220351	Sequence
38	140.8	5.4	1275	6	AX088102	Sequence
39	140.8	5.4	1297	8	BT009276	Triticum
40	140.8	5.4	3386	8	AY044844	Triticum
41	137.6	5.3	759	6	AX756331	Sequence
42	134.4	5.2	2748	8	AY224560	Orzya sat
43	134.4	5.2	3080	8	AX373258	Orzya sat
44	134.4	5.2	3280	8	AK067577	Orzya sat
45	125.2	4.8	2865	6	AX654024	Sequence

ALIGNMENTS

RESULT 1

AR085480

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

AR085480

Sequence 1 from patent US 5981728.

AR085480

AR085480.1 GI:10012247

Unknown.

Unknown.

Unclassified.

1 (bases 1 to 6027)

Myers, A.M. and James, M.G.

Dulll coding for a novel starch synthase and uses thereof

Patent: US 5981728-A 1 09-NOV-1999;

Location/Qualifiers

6027 bp

DNA

linear

FAT 01-SEP-2000

parent

source	1. .6027	/organism="unknown"	/mol_type="unassigned DNA"
ORIGIN			
Query Match	100.0%;	Score 2598;	DB 6; Length 6027;
Best Local Similarity	100.0%;	Pred. No. 0;	
Matches 2598;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	AGCTTGCTGAAAAAATATTTCGCTGGAAACAAGTTGTTTACTATTCCAGATGATGA	60
Db	2425	AGCTTGCTGAAAAAATATTTCGCTGGAAACAAGTTGTTTACTATTCCAGATGATGA	2484
QY	61	AAGCTGATTCACAAATGATCTCTATTTCATTCGTGATCTATCAGCTGCGCCAAATGAGC	120
Db	2485	AAGCTGATTCACAAATGATCTCTATTTCATTCGTGATCTATCAGCTGCGCCAAATGAGC	2544
QY	121	CTGATGTACTTATCAAAAGGAGCATTCATAGGGTGGAAAGTGAGATTTTTCACCTGAAAAAT	180
Db	2545	CTGATGTACTTATCAAAAGGAGCATTCATAGGGTGGAAAGTGAGATTTTTCACCTGAAAAAT	2604
QY	181	TGCACAAAGCGAGCTCGCAGGGGACCTGGTGGCTGCTGCAAACTATACATTCCTTAAGCAGG	240
Db	2605	TGCACAAAGCGAGCTCGCAGGGGACCTGGTGGCTGCTGCAAACTATACATTCCTTAAGCAGG	2664
QY	241	CATACAGAAATGGACTTGTGTTTTTAAACGACACACGGTATATGAAAAATAAACAATA	300
Db	2665	CATACAGAAATGGACTTGTGTTTTTAAACGACACACGGTATATGAAAAATAAACAATA	2724
QY	301	ATGATTTTCGTGATACAAATAGAAAGCACCATGGATGAAAAATTTATTTGAGGATTTCTTGG	360
Db	2725	ATGATTTTCGTGATACAAATAGAAAGCACCATGGATGAAAAATTTATTTGAGGATTTCTTGG	2784
QY	361	CTGAGAAAGCAACGAGAACTTGCAGAACCTTGCCAATGAGGAGCTGCAAGGAGGAGAC	420
Db	2785	CTGAGAAAGCAACGAGAACTTGCAGAACCTTGCCAATGAGGAGCTGCAAGGAGGAGAC	2844
QY	421	AAACTGATGACGACGGCGAATGAGGAAGAAAGGGCGGCAGATAAAAGCTGACAGGGTAC	480
Db	2845	AAACTGATGACGACGGCGAATGAGGAAGAAAGGGCGGCAGATAAAAGCTGACAGGGTAC	2904
QY	481	AAGCCAAAGTTGAGGTAGACGAGGAAGAAATAATTTGTGCAATGTATTTGGGTTTAGCCA	540
Db	2905	AAGCCAAAGTTGAGGTAGACGAGGAAGAAATAATTTGTGCAATGTATTTGGGTTTAGCCA	2964
QY	541	GAGCTCCTGTTGATAATTTATGTGTACATTTGAGCCCATCAGACCTGGCAAGAGGCTACTG	600
Db	2965	GAGCTCCTGTTGATAATTTATGTGTACATTTGAGCCCATCAGACCTGGCAAGAGGCTACTG	3024
QY	601	TCAGATTGTATTAATAACATAAACTCAAGACCTCTAGTTCACAGTACTGAGATATGATATGC	660
Db	3025	TCAGATTGTATTAATAACATAAACTCAAGACCTCTAGTTCACAGTACTGAGATATGATATGC	3084
QY	661	ATGCTGCTATAACAAATGGATTGATGGACTCTCTTTTGCCTGAAGGCTCTTTCATCATC	720
Db	3085	ATGCTGCTATAACAAATGGATTGATGGACTCTCTTTTGCCTGAAGGCTCTTTCATCATC	3144
QY	721	ATGACAAAGATTGTGATTTGGTGGTTTGCAGATGTTTGTCTGCTGCCTGAAAGACATATGAT	780
Db	3145	ATGACAAAGATTGTGATTTGGTGGTTTGCAGATGTTTGTCTGCTGCCTGAAAGACATATGAT	3204
QY	781	TGGAATCGGTTTTTGTGACGGCCCAACAGGAGGTGCAAGGAATATGACAAACATATGAG	840
Db	3205	TGGAATCGGTTTTTGTGACGGCCCAACAGGAGGTGCAAGGAATATGACAAACATATGAG	3264
QY	841	GACATGATTTTCATGCTACCTTCCAAATAACATGACTGAGGAAGATTTTGGATGGAG	900
Db	3265	GACATGATTTTCATGCTACCTTCCAAATAACATGACTGAGGAAGATTTTGGATGGAG	3324
QY	901	AAGAACAAAGGATCTATAAAGGCTTCAACAGGAGGAGGGAAGGGAGGAGGCTATTTA	960
Db	3325	AAGAACAAAGGATCTATAAAGGCTTCAACAGGAGGAGGGAAGGGAGGAGGCTATTTA	3384

dl1

Db 4705 ATACGCTCCACGCGCTAAACCATGGCAAGTGGAGCTTCCTTGACCTAGACGACCTC 4764
QY 2341 TCTCGCATCTGATATACGCTGGCTCTGACTTCACTTCTGGTCCCATCATATTTGAGCCTT 2400
Db 4765 TCTCGCATCTGATATACGCTGGCTCTGACTTCACTTCTGGTCCCATCATATTTGAGCCTT 4824
QY 2401 GCGGCTTAACCTAGCTGCTGCCATCGGCTATGGAACCATCCCGATTGTCGCAAGACTG 2460
Db 4825 GCGGCTTAACCTAGCTGCTGCCATCGGCTATGGAACCATCCCGATTGTCGCAAGACTG 4884
QY 2461 GAGGCTCTTCGACACTGCTCTCGATGTCGACCAATGACAAAGCAAGCCCGAGATCGAG 2520
Db 4885 GAGGCTCTTCGACACTGCTCTCGATGTCGACCAATGACAAAGCAAGCCCGAGATCGAG 4944
QY 2521 GCCTTGAGCCCAACGGGTTTGTAGCTTTCACGAGCTGATGACCAAGCTGTTGACTACGCGC 2580
Db 4945 GCCTTGAGCCCAACGGGTTTGTAGCTTTCACGAGCTGATGACCAAGCTGTTGACTACGCGC 5004
QY 2581 TGAACAGGCGGATCTCAG 2598
Db 5005 TGAACAGGCGGATCTCAG 5022

RESULT 4
AF023159
LOCUS Zea mays starch synthase DULL1 (dull1) mRNA, complete cds.
DEFINITION Zea mays starch synthase DULL1 (dull1) mRNA, complete cds.
ACCESSION AF023159
VERSION AF023159.1 GI:3057119
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 6027)
Gao, M., Wanat, J., Stinard, P.S., James, M.G. and Myers, A.M.
Characterization of dull1, a maize gene coding for a novel starch
synthase
Plant Cell 10 (3), 399-412 (1998)
MEDLINE 98169346
PUBMED 9501113
2 (bases 1 to 6027)
Gao, M., James, M.G. and Myers, A.M.
Direct Submission
Submitted (06-SEP-1997) Biochemistry & Biophysics, Iowa State
University, 2152 Molecular Biology Building, Ames, IA 50011, USA
Location/Qualifiers
1. 6027
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
/chromosome="10"
1. 6027
/gene="dull1"
/allele="wild type"
120..5144
/gene="dull1"
/note="similar to potato starch synthase SSIII; likely to
be the maize starch synthase defined biochemically as
SSII"
/codon_start=1
/product="starch synthase DULL1"
/protein_id="AAC14014.1"
/db_xref="GI:3057120"
translation="MEMVLRSSQPLCLRSGPVLIFRPTVAGGGGQSLRTRFARR
RIVRCVAGPCNKRSTASPNVKVAYSNYAPRLLVSSKSEHSDSSRREFTI
DIVNGLSGSDAALTSNRDVEIQLHI SEELPGKV INASLGEMETVDEAVEED
KEVDTSGLVLRNVAAREVDPKDEHNAKDVFVDSGSTAPDNAVEEVVDEAVEEDM
VDVILGLNNATIEIDIMEALLEENFDVSPGNASSGRTYGGVDELGELPSTSD
CTAINGKRSLKPLPIVRFOEQEQLVSI VDEEGLIASSCEEGFVVDVYDKQENS
TAFDEQQLTDFPEEGISIVHFPEENNDIVSGSELEQKDELDSYKODRSTGLHE
QDQSVSSHQKSI VGVPPQIQNDQSIAGSHRQDQSIAGAEQIQSVAGYIKPNQS

too late

ORIGIN

Query Match 100.0%; Score 2598; DB 8; Length 6027;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTTGTGAAATAATATTTCGCTGGAAACAGTGTCTTACTTATCCAGATGATTGA 60
Db 2425 AGCTTGTGAAATAATATTTCGCTGGAAACAGTGTCTTACTTATCCAGATGATTGA 2484
QY 61 AAGCTGATTCACAAATGATCTCTATTTCATCTGATCTATCATGCTGTGCCAATGAGC 120
Db 2485 AAGCTGATTCACAAATGATCTCTATTTCATCTGATCTATCATGCTGTGCCAATGAGC 2544
QY 121 CTGATGACTTATCAAAGGAGCATTCATGGTGGAGAGTGGAGATTTTCTACAGAAAAT 180
Db 2545 CTGATGACTTATCAAAGGAGCATTCATGGTGGAGAGTGGAGATTTTCTACAGAAAAT 2604
QY 181 TGCACAGAGCGAGCTGCGAGGGGACTTGGTGGTCTGCAAACTATACATTCCTAAGCAGG 240
Db 2605 TGCACAGAGCGAGCTGCGAGGGGACTTGGTGGTCTGCAAACTATACATTCCTAAGCAGG 2664
QY 241 CATACAGAAATGAGCTTTGTGTTTTTAAACGACACACGGTATGAAATAATACAAATA 300
Db 2665 CATACAGAAATGAGCTTTGTGTTTTTAAACGACACACGGTATGAAATAATACAAATA 2724
QY 301 ATGATTCGTGATACAAATAGAAAGACCATGGATGAAATTTTATTCAGGATTTCTTGG 360
Db 2725 ATGATTCGTGATACAAATAGAAAGACCATGGATGAAATTTTATTCAGGATTTCTTGG 2784
QY 361 CTGAAGAAAGCAACGAGAACTTCAGAACTTGCACAACTGAGAAAGCTGAAAGGAGGAGAC 420
Db 2785 CTGAAGAAAGCAACGAGAACTTCAGAACTTGCACAACTGAGAAAGCTGAAAGGAGGAGAC 2844
QY 421 AAACCTGATGACAGCGCGCAATGGAGGAAAGAAAGGGCGCGAGATAAGCTGACAGGGTAC 480
Db 2845 AAACCTGATGACAGCGCGCAATGGAGGAAAGAAAGGGCGCGAGATAAGCTGACAGGGTAC 2904
QY 481 AAGCCAAAGTTGAGGTAGACGACGAGAGAGAGTAATTTGTCGAATGATTTGGTTTAGCCA 540
Db 2905 AAGCCAAAGTTGAGGTAGACGACGAGAGAGAGTAATTTGTCGAATGATTTGGTTTAGCCA 2964
QY 541 GAGCTCCCTGTTGATAATTTATGGTATTCATTCAGCCCATCAGACTGCGAAGAGGCTACTG 600
Db 2965 GAGCTCCCTGTTGATAATTTATGGTATTCATTCAGCCCATCAGACTGCGAAGAGGCTACTG 3024
QY 601 TCAGATGCTTATTAACATAAACTCAAGACCTCTTCTAGTTCAAGTACTGAGATATGATGC 660
Db 3025 TCAGATGCTTATTAACATAAACTCAAGACCTCTTCTAGTTCAAGTACTGAGATATGATGC 3084
QY 661 ATGGTGGCTATTAACAAATGGATGATGAGTCTCTTTCTGCTGAAAGGCTTGTTCATCATC 720

Db	3085		ATGTGGCTATAACAAATGGATTTGATGGACTCTCTTTTCTGTAAGGCTTGTTTCATCATC	3144
QY	721		ATGACAAAGATTGTGATTGGTGGTTTGCAGATGTTGTCTGCTGCTGAAAGAACATATGTTAT	780
Db	3145		ATGACAAAGATTGTGATTGGTGGTTTGCAGATGTTGTCTGCTGCTGAAAGAACATATGTTAT	3204
QY	781		TGGACTGGGTTTTTCTGTACGGGCCCAACAGGAGTGCAGAGGAATTATGACAACAATGGAG	840
Db	3205		TGGACTGGGTTTTTCTGTACGGGCCCAACAGGAGTGCAGAGGAATTATGACAACAATGGAG	3264
QY	841		GACATGATTTTTCATGCTACCCCTCCAAATAACATGACTGAGGAAGAGTATTGGATGGAAG	900
Db	3265		GACATGATTTTTCATGCTACCCCTCCAAATAACATGACTGAGGAAGAGTATTGGATGGAAG	3324
QY	901		AAGAACAAAGGATCTATACAAGGCTTCAACAGAGAGGAGGGGAAAGGAGGAGGCTATTTA	960
Db	3325		AAGAACAAAGGATCTATACAAGGCTTCAACAGAGAGGAGGGGAAAGGAGGAGGCTATTTA	3384
QY	961		AAAGGAAGGCTGAGAGAAATGCAAAAATGAAAAGCTGAGATGAAGGAAGACATATGAGAA	1020
Db	3385		AAAGGAAGGCTGAGAGAAATGCAAAAATGAAAAGCTGAGATGAAGGAAGACATATGAGAA	3444
QY	1021		TGTTCTGCTGTTTCTCAGAAACACATTTTACACCGAACACATTTGAAATACATGCTCGAA	1080
Db	3445		TGTTCTGCTGTTTCTCAGAAACACATTTTACACCGAACACATTTGAAATACATGCTCGAA	3504
QY	1081		CTACTATTGATGTGCTTTTATAATCCCTTCTAATCAGTTCTAACTGGAAAGCCAGAGTTT	1140
Db	3505		CTACTATTGATGTGCTTTTATAATCCCTTCTAATCAGTTCTAACTGGAAAGCCAGAGTTT	3564
QY	1141		GGTTTCGATGTTCTCTTAATTCGTTGGATGTTATCCAGTGGGGTGTGCCACTCAGAA	1200
Db	3565		GGTTTCGATGTTCTCTTAATTCGTTGGATGTTATCCAGTGGGGTGTGCCACTCAGAA	3624
QY	1201		TGTTCAAGCAGAAATGTTTACACCTTAAAGCAACAGTTTACGTTCCAGAGATGCTT	1260
Db	3625		TGTTCAAGCAGAAATGTTTACACCTTAAAGCAACAGTTTACGTTCCAGAGATGCTT	3684
QY	1261		ATATGATGGACTTCGTTTTCTCGGAGTCAGAAAGGTGGAAATTTATGATTAACAGAAATG	1320
Db	3685		ATATGATGGACTTCGTTTTCTCGGAGTCAGAAAGGTGGAAATTTATGATTAACAGAAATG	3744
QY	1321		GGTTPAGACTATCATATTCCTGTTTTGGGTCAAATTGCAAGAACCACTATGCACATG	1380
Db	3745		GGTTPAGACTATCATATTCCTGTTTTGGGTCAAATTGCAAGAACCACTATGCACATG	3804
QY	1381		TCCACATGCTGTTTGAGATGACCAATCGCAAGAGTTGGAGGTCTTGGTGAATGTTGTCA	1440
Db	3805		TCCACATGCTGTTTGAGATGACCAATCGCAAGAGTTGGAGGTCTTGGTGAATGTTGTCA	3864
QY	1441		CTAGTCTTTACGTCCTGTGCAAGATTTAGGACACAATGTGAGGTTATTCTTCCAAAGT	1500
Db	3865		CTAGTCTTTACGTCCTGTGCAAGATTTAGGACACAATGTGAGGTTATTCTTCCAAAGT	3924
QY	1501		ACGTTGCTTGAATCTAAGCAATGTCAAGAATCTCAAAATCCATCAGATTTTCTTGGG	1560
Db	3925		ACGTTGCTTGAATCTAAGCAATGTCAAGAATCTCAAAATCCATCAGATTTTCTTGGG	3984
QY	1561		GTGGTCTGAAATAAATGTGCGGTGGACTAGTCCAAAGGCTTTCTGTTTACTTCTCTGG	1620
Db	3985		GTGGTCTGAAATAAATGTGCGGTGGACTAGTCCAAAGGCTTTCTGTTTACTTCTCTGG	4044
QY	1621		AACCTCAAAATGGGATGTTTGGAGTCGGATATGTATATGTCACGGACGATGACCGCGAT	1680
Db	4045		AACCTCAAAATGGGATGTTTGGAGTCGGATATGTATATGTCACGGACGATGACCGCGAT	4104
QY	1681		TTGGCTCTTCTGTGCTGTCTAGAGTTTCTTCTCCTCAAGTGGATCTTCTCCGAA	1740
Db	4105		TTGGCTCTTCTGTGCTGTCTAGAGTTTCTTCTCCTCAAGTGGATCTTCTCCGAA	4164
QY	1741		TAATACATTGCCATGATTGGTCAAGTCTCTGCTGCTGGCTACCAAGAAACTACG	1800

Db	4165	TAATACATTTGCCATGATTGGTCAAGTGTCTCTGTTGGCTTGCGGTACACAAAGGAAACTACG	4224
Qy	1801	CGAAGTCTAGCTTTGGCAAAACGACGGGTGGTATTCAACATCCACAATCTTGATTTTGGAG	1860
Db	4225	CGAAGTCTAGCTTTGCAAAAGCACGGGTGGTATTCAACATCCACAATCTTGATTTTGGAG	4284
Qy	1861	CGCATCATATTGGCAAAAGCAATAGANATTGTGTATTAAGCAACAACCTGTCTCTTAATACAT	1920
Db	4285	CGCATCATATTGGCAAAAGCAATAGANATTGTGTATTAAGCAACAATGTCTCTTAATACAT	4344
Qy	1921	ATTCAAAGGAAGTGTCAAGTCTATGTTGCCATAGTTCCCTCATCTTGGGAAATTTATGGCA	1980
Db	4345	ATTCAAAGGAAGTGTCAAGTCTATGTTGCCATAGTTCCCTCATCTTGGGAAATTTATGGCA	4404
Qy	1981	TTTCTCAATGGAAATGGATCCGGATATATGGGATCCGTACAATGACAACTTTATCCCGTCC	2040
Db	4405	TTTCTCAATGGAAATGGATCCGGATATATGGGATCCGTACAATGACAACTTTATCCCGTCC	4464
Qy	2041	ACTACACTTTGTGAGAAATGTGGTTGAAGGCAAGAGGGCTGTAAAGAGGCACTGCAGCAGA	2100
Db	4465	ACTACACTTTGTGAGAAATGTGGTTGAAGGCAAGAGGGCTGTAAAGAGGCACTGCAGCAGA	4524
Qy	2101	AGTTTGGGTTTACAGCAAAATCGATGTCCCCTGCTAGGAATCGTCACTCGCCTGCAGCCC	2160
Db	4525	AGTTTGGGTTTACAGCAAAATCGATGTCCCCTGCTAGGAATCGTCACTCGCCTGCAGCCC	4584
Qy	2161	AAAAGGGGATCCACTGATCAAGCATCGGATTCACCGTACACTCGAAGCGGAACGCACAGG	2220
Db	4585	AAAAGGGGATCCACTGATCAAGCATCGGATTCACCGTACACTCGAAGCGGAACGCACAGG	4644
Qy	2221	TGGTTTGTCTTGGTTTCAGCGCCCGGACTCTCGAATCCCAAGCTGATTTGTCAACTGGCGA	2280
Db	4645	TGGTTTGTCTTGGTTTCAGCGCCCGGACTCTCGAATCCCAAGCTGATTTGTCAACTGGCGA	4704
Qy	2281	ATACGCTCCACGGCGTAAACCATGGGCAGATGAGGCTTTCCCTGACCTACGACGAGCCTC	2340
Db	4705	ATACGCTCCACGGCGTAAACCATGGGCAGATGAGGCTTTCCCTGACCTACGACGAGCCTC	4764
Qy	2341	TCTCGCATCTGATATACGCTGGGCTGACTTCATTCTGGTCCCATCTATATTGAGCCTT	2400
Db	4765	TCTCGCATCTGATATACGCTGGGCTGACTTCATTCTGGTCCCATCTATATTGAGCCTT	4824
Qy	2401	GCGGCCCTAACTCAGCTCGTCCGCCATGGGGTATGMAACCATCCGATATGTCGCAAGACTG	2460
Db	4825	GCGGCCCTAACTCAGCTCGTCCGCCATGGGGTATGMAACCATCCGATATGTCGCAAGACTG	4884
Qy	2461	GAGGGCTTTCCGACACTGTCTTCCGATGTGGACATGACAAAGAAACGAGCCGAGATCCGAG	2520
Db	4885	GAGGGCTTTCCGACACTGTCTTCCGATGTGGACATGACAAAGAAACGAGCCGAGATCCGAG	4944
Qy	2521	GCCTTGAGCCCAACGGGTTTAGCTTTGACGGAGCTGATAGCAACCGTGTGTGACTACGGCC	2580
Db	4945	GCCTTGAGCCCAACGGGTTTAGCTTTGACGGAGCTGATAGCAACCGTGTGTGACTACGGCC	5004
Qy	2581	TGAACAGGGCGATCTCAG	2598
Db	5005	TGAACAGGGCGATCTCAG	5022

RESULT 5	AF258608	5346 bp	linear	PLN 27-JUL-2000
LOCUS	AF258608			
DEFINITION	Triticum aestivum starch synthase III mRNA, complete cds.			
ACCESSION	AF258608			
VERSION	AF258608.1	GI:9502142		
KEYWORDS	.			
SOURCE	Triticum aestivum (bread wheat)			
ORGANISM	Triticum aestivum			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliopsida; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.			
REFERENCE	1. (bases 1 to 5346)			
AUTHORS	Li, Z., Mouille, G., Kesar-Hashemi, B., Rahman, S., Clarke, B.,			

Gale, K.R., Appels, R. and Morell, M.K.
The structure and expression of the wheat starch synthase III gene.
Motifs in the expressed gene define the lineage of the starch
Synthase III gene family
Plant Physiol. 123 (2), 613-624 (2000)
20317203
10859191
REFERENCE
2 (bases 1 to 5346)
Li, Z., Mouille, G., Kosar-Hadshemi, B., Rahman, S., Clarke, B.,
Gale, K.R., Appels, R. and Morell, M.K.
Direct Submission
Submitted (19-APR-2000) CSIRO Division of Plant Industry, GPO Box
1600, Canberra, ACT 2601, Australia
Location/Qualifiers
1. 5346
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/chromosome="1"
29. 4915
/note="WSSI11"
/codon_start=1
/product="starch synthase III"
/protein_id="AAF87999.1"
/db_xref="GI:9502143"
/translation="MEMSLWPSPLCPRSRQPLVVRPAGRGGLQTPFLMNGRFRSR
TLRCVAGSDPNNRKRMRVPPQVKVVISRGYVTRLIIVPSNTEHNRDEETLDY
NALLSTAEWDDNREAEAKADSSONALSSIIIEVDVADDEIIAALDLYVLSLV
KEVDAAAKARVKEAFELDLPAITRSIVIVDMHNGTVQETLSRIVIVDMHNGTV
QETLSRIVIVDMHNGTVQETLSRIVIVDMHNGTVQETLSRIVIVDMHNGTVQETLSR
TSSGNVSNATVREDADEAGNDQCI FRADLSGNVFSSTVEVGADEAGSIKDRF
FAMDLPFASGHEKIMADVQADDEETVQOQVPPSSRSMKDAKATGVSNLPE
LRLVVEQKGVNFSKDKSLDDLPQGNOSIIGSVKODKSIADVAGTQSFSGSKQ
HRSIVAFKQNSIVSVTEQKSIIVGPSQSLSAVSLKQNPVIVGTREGGQTKQPV
VDRQALVNGLEAKGERTSEKTDALHVKFNVDNLRHQADTQAVEKTKQV
DEHLYMTEHOKRAAGQVNVNDELSITEIGMRGDKIQHVLSEELSWSEDEVLQI
EDDQYEVDETVSVYVNDQIIGSPQDVVDPQALQMLQELAEKNYSNRNKLFPVPEV
VKADSVIIDLNRDLTALANEEDVVIKGFNGKWRLLFTLRHSLDLGVMWSKLEYI
PKEAVRLDPVFNPTVYNNNGNDFCI GLEGTWNEDELPEOPLVKEKQRELEKAME
AERRTQTEORRKEARADEAVRAQAKAEI KKKLQSLSLARTCVNMLYLEAS
TDRTGTLRLYNRNSRPLAHSITELMHGYNNTDGLSIVSFVKCDKQDGMWYAD
VIPPKEALVLDVADGPNARNYNNARQDFHAILPNNNVTEEGFWAQEEQNIYTR
LLOERREKEMTKRKAESANIKAEKAKWRFLLSKHIVYTEPLIRAGTQVVDVL
YNPSNTVLNGSEKGFRCFNLHMSGALPQKMKVSGDGLLAKTVDVDPDAVMD
VFSEWEDGIYDNRGMDYHIVPDSITETENYMERI IHAIVEMA PVAKVGLGVVTS
LSRATQDLIGHTVVEVL PKVDCINQSVKDLHLIQSFSGGTEIKVWGRVEDLVYFL
EPONGMFGVGVYGNDRRRGFCHSALEFILQNEFSPIIICHWSAPVAMLYKE
HYSQSRMASTRVFTIHLNLFQGHVYIGKAMTYCDKATTVSPYSDRVAGHGAIAFPHRE
KPYGLLIDDPIDPDYNDNFIPIVPTCENVVEGRKRAALQKQFGLQOTDVPVIGI
ITRLTAQKGIHLIKHAIHRTLESNGVLLGAPDRIQGDPCRLADALHGVYHGRVK
LVLYDEPLSHLIYAGSDFIIVPSIFPEPGLTOLVAMRYGSIPIVRYKTHGLHDTVDV
DNDKDRSLGLEPNEGFSFGDNGVDYALNRAICAMFARDNDFHSLCKRMQEDWS
WNRPALDIYELHARKE"

Query Match 68.0%; Score 1766.6; DB 8; Length 5346;
Best Local Similarity 80.3%; Pred. No. 0;
Matches 2085; Conservative 509; Indels 3; Gaps 1;
QY 1 AGCTTGCTGAAAAAATATTGCTGGGAACAACAGTTGTTACTTATCCAGATGATTGA 60
DB 2193 AACTCGCTGAGAAAAATATTTCGATGAGAAACAAGCTGTTGTTTTCAGAGGTAGTGA 2252
QY 61 AAGCTGATTCAACAATTCATCTCTATTTCAATCGTGATCTACCTGCTGGCCATGAGC 120
DB 2253 AAGCTGATTCACTATTGATCTTTATTTAAATCTGACCTAACAGCTTTGGCGAATGAAC 2312
QY 121 CTGATGTAATCAAGAGCATTCAATGGGTGGAAGTGGAGATTTTCACTGAAAAAT 180
DB 2313 CCGATGTCGTCATCAAGAGCATTCAATGGTGGAAATGGAGGCTTTTCACTGAAAGAT 2372
QY 181 TGCACAAGCGAGCTGCGAGGGGACTGGTGGTGTGCTCAAACTATACATTCCTAAGCAGG 240

2373 TGCAACAAGAGTACCTTGAGGGGTTTGGTGTCTTTGCAAACTGTACATACCAAGGAGG 2432
QY 241 CATACAGAAATGACATTTGTGTTTTTAAACGACACACCGGTATATGAAAAATAATAACAATA 300
DB 2433 CCTACAGATTAGACTTTGTGTTCTTCAACGGTTCGACGGTCTATGAGAACAAATGGAACA 2492
QY 301 ATGATTTCGTGTATCAAAATAGAAAGCACATGGATGAAATAATTTATTGAGGATTTCTTGG 360
DB 2493 ATGATTTCGTGTATGGAATAGAAAGCACTATGAATGAAGATCTGTTGAGGATTTCTTGG 2552
QY 361 CTGAAGAAAGCAACGAGAACCTTGAGAACCTTGCAATGAGGAAGCTGAAAGAGGAGAC 420
DB 2553 TTAAGAAAGCAAGGAGGCTTTGAGAACTTGGCCATGGAAGAGCTGAAAGAGGAGAC 2612
QY 421 AAACCTGATGAGCAGCGCGCAATTGAAGAAAGGCGCGCAGATAAAGCTGACAGGGTAC 480
DB 2613 AGACTGAAGAACAGCGCGCGAAGAAAGGAGGAGGCTGCGAGATGAAGCTGTCAAGGAC 2672
QY 481 AAGCCAAAGGTTGAGTAGAGACGAGAAAGAAATAATTTGTGCAATGTTATGGGTTTAGCCA 540
DB 2673 AAGCGAAGCGCGAGATGAGATCAAGAAAGAAATAATTTGAAAGTATGTTGAGTTTGGCCA 2732
QY 541 GAGCTCCCTGTTGATTAATTTATGTTGATGACCTGAGCCCATCAGACTGACAGAGGCTACTG 600
DB 2733 GAACATGTTGATTAATTTGTTGATGAGGCTGACAGATCAAGAGGAGATCTA 2792
QY 601 TCAGATTCTATTATAACATAAACTCAAGACCTCTAGTTTCAAGACTGAGATATGATGATG 660
DB 2793 TCAGGTTATTATTAACAGAACTCGAGGCCACTTGGCGCATAGTACTGAGATTGGATGC 2852
QY 661 ATGGTGGCTATAACAAATTTGATGATGACACTCTTTTGTCTGAAAGGCTTGTTCATCATC 720
DB 2853 ATGGTGGTTTAAACAATTTGAGCAGATGAGCACTCTTANTTTTGAAGGCTTTGTCAAGTGA 2912
QY 721 ATGACAAAAGATTGTGATTTGGTGGTGTGAGATGTTGTCGCTGCTGAAAGACATATGAT 780
DB 2913 ATGACAAAAGACGGCGATTGTTGGTGTATGCAAGTATTTTCACCTGAAAGGCACTTTGT 2972
QY 781 TGGACTGGGTTTTGCTGACGGCCCAACGAGGAGTGCAGGAATTTATGACAACTATGAG 840
DB 2973 TGGACTGGGTTTTGCTGATGGCGCAGCTGGGAAATGCAAGAACTATGACAACTATGCTC 3032
QY 841 GACATGATTTTCATGCTACCTTCCAAATAACA --- TCACCTGAGGAAGAGTATGATGATG 897
DB 3033 GACAAAGATTTTCATGCTATTTCTTCGAAACAATAATGTAACCGAGGAGGCTTCTGGCGC 3092
QY 898 AAGAGAAACAAAGGATCTATACAAGGCTTCAACAGAGAGGAGGAGGAGGAGGCTA 957
DB 3093 AAGAGGACAAAACATCTATACAAGGCTTCTGCAAGAAAGAGAGAGAAAGAGAAACA 3152
QY 958 TTAAGAGAGGCTGAGAGAAATGCAAAATGAAAGCTGAGATGAAGGAAAGAGTATGA 1017
DB 3153 TCAAAAGAAAGGCTGAGAGAAAGTCAAAATATCAAAAGCTGAGATGAAGGCAAAACATATG 3212
QY 1018 GAATGTTCTCTGTTTCTCAGAAACACATTTGTTTACACGACCACTTCAATACATGCTG 1077
DB 3213 GAAGTTTCTCTCTCCAGAAACACATTTGTTTATACGAAACCCCTTGAATATGCTGCGC 3272
QY 1078 GAACCTACTATTGATGCTGTTTATTAATCTCTTAATACAGTTCTAACTGAAAGCCAGAGG 1137
DB 3273 GAACCAAGTGTGATGCTATACAAATCCCTCTACACAGTCTTAAATGGAAGTTCGAGG 3332
QY 1138 TTTGGTTTCGATGTTCTTTTAATCGTTGATGATCCAGTGGGGTGTTCACCTCAG 1197
DB 3333 GTTGGTTTAGATGCTCTCTTTAACTTTGGATGCAATCAAGTGGGGCATTTGCCACCCACA 3392
QY 1198 AGATGGTACAGCAAGAAATGTTTCACACCTTAAAGCAACAGTTTACGTTCCACGAGATG 1257
DB 3393 AGATGGTGAATACAGGGGATGGGCGCTCTTTAAAGCAACAGTTGATGTTCCACCGGATG 3452
QY 1258 CCTATATGAGGACTCGTTTCTTCGGAGTCAGAAAGAGGTGGAATTTATGATACAGAA 1317

ORIGIN

3453 CCTATATGATGACCTTTGTTTCTCCGAGTGGAGAAATGGGATCTATGACAACAGCA 3512
1318 ATGGGTTAGACTATCATATCTCTGTTTGGGTTCAATTCGAAAGGAACACCTATGACACA 1377
3513 ATGGGATGACTATCATATCTCTGTTTCTGATTCATTTGAAACAGAGAATTCATGCGTA 3572
1378 TTGTCCACATTCGCTGTGAGATGGACCAATCGCAAGGTTGGAGTCTTGTGATGTG 1437
3573 TTATCCACATTCGCTGTGAGATGGCCCCGTTGCAAGGTTGGAGTCTTGGGATGTG 3632
1438 TCACCTAGTCTTTCACGCTGTGCAAGATTTAGGACACAATGTGAGGTTATTTCTCCAA 1497
3633 TTACAAGTCTTTCACGCTGCAATTCAGATCTAGGACATCTGCGAGTTATCTCCGA 3692
1498 AGTACGGTTGCTTGAATCTAAGCAATGTCAAGATCTCAAAATCCATCAGAGTTTCTTT 1557
3693 AGTACGACTGTTTGAACCAAGCAGTGTCAAGGATTTACATTTATATCAAGGTTTCTTT 3752
1558 GGGGTGGTTCTGAATAAATGTGCGGTGGACTAGTCGAAGGCCCTTTGTGTTTACTTCC 1617
3753 GGGGTGGTTACAGAAATPAAAGTANGGTTGGAGTCCGAGACCTGACCGTTTACTTCC 3812
1618 TGGAACTCTCAAAATGGGATGTTTGGAGTCCGATATGATATGSCAGGACGATACCGCC 1677
3813 TGGAACTCTCAAAATGGGATGTTTGGCGTTGGATGTGATATGGAAGGATGATACCGCA 3872
1678 GATTGGCTTCTTCTGCTGCTCTAGAGTTTCTCTCCMAAGTGAATCTTCCGA 1737
3873 GATTGGGTTCTTCTGCTGCTCTAGAGTTTCTCTCCMAAGTGAATCTTCTCCAC 3932
1738 ACATATACTATGCCATGATGTTGCTCAAGTCTCTGCTGCTGGCTACACAAGGAAACT 1797
3933 ATATATACTATGCCATGATGTTGCTCAAGTCTCTGCTGCTGGCTACACAAGGAAACT 3992
1798 AGCGAAGTCTAGCTTGGCAAGCGCAAGGTTGATTTCCACATCCCAATCTTGAATTTG 1857
3993 ATTCCCACTCCAGATGGCAAGCACTCGGTTGATTTTACCATCCCAATCTTGAATTTG 4052
1858 GAGCGCATATATGGCAAGCAAGCAATGATATGATATGATTAAGCAACATCTCTTAATA 1917
4053 GAGCATATATATGGCAAGCAAGCAATGATATGATATGATTAAGCAACATCTCTTCTTA 4112
1918 CATATTCAGGAAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1977
4113 CATATTCAGGAAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4172
1978 GATTTCTCAATGGAATGTATCCGATATATGAGTCCGATCCGATCCGATCCGATCCGAT 2037
4173 GATTTCTCAATGGAATGTATCCGATATATGAGTCCGATCCGATCCGATCCGATCCGAT 4232
2038 TCCACTACATTTGTGAGATGTTGTGAAGGCAAGAGGCTGCTAGAGGGCACTGCGAC 2097
4233 TCCCTTATCTTGTGAGATGTTGTGAAGGCAAGAGGCTGCTAGAGGGCACTGCGAC 4292
2098 AGAAGTTTGGGTTTACAGCAATTCGATGCTCCGCTGCTAGGAAATCGTCACTCGCTGACAG 2157
4293 AGAAGTTTGGATTTACAGCAATTCGATGCTCCGCTGCTAGGAAATCGTCACTCGCTGACAG 4352
2158 CCGAAAGGGGATTCACCTGATCAAGCATGCGATTCACCGTACATCTCGAATCATCAACCGT 2217
4353 CCGAAGGGGATTCACCTGATCAAGCATGCGATTCACCGTACATCTCGAATCATCAACCGT 4412
2218 AGTGTGTTTGTGTTTGTGCTCAGGCGCGGCTCTCGAATCCAGCTGATTTTGTCAACTCG 2277
4413 ATGTGTTTGTGTTTGTGCTCAGGCGCGGCTCTCGAATCCAGCTGATTTTGTCAACTCG 4472
2278 CGAATACGCTCCACCGGCTAAACCATGGGCAAGTGGGCTTTCTTGTGCTAGCAGCAGC 2337
4473 CCGATGCTCTCTCATGTTTACCATGTTAGGTTGAAGTCTTCTTAACTTATGATGAGC 4532
2338 CTCTCTCGCATCTGATATGAGTGTGCTCTGATCTTCAATCTGCTGCTCCATCTATTTGAGC 2397
4533 CTCTTCTCAGCTGATATACGCTGGCTCGGACTTCTATATTTGTTCTTCAATCTTCCGAC 4592

QY 2398 CTGCGGCTTAATCTAGCTCTGCTGCGCATGCGGTATGGAACCATCCGATGTCGCAAGA 2457
Db 4593 CCGTGGCTTAAACAACATGTTGCGCATGCGGTATGGAATCGATCCCTATAGTTCGAAAA 4652
QY 2458 CTGAGGGCTCTTCGACACTGCTTCGATGTCGCAATGACAAGGAACGAGCCGAGATC 2517
Db 4653 CTGAGGACTCTTCGACACACAGTCTTCGAGTGAACAATGAAGACCGGCTCGTCTC 4712
QY 2518 GAGGCTTTGAGCCCAACGGGTTTAGCTTTGACGAGCTGATGCAACGGTGTGACTAG 2577
Db 4713 TTGGTCTTGAACCAATGGGTTTCAGTTTCGACGAGCCGACAGCAATGCGTGGATTATG 4772
QY 2578 CGCTGAACAGGGCGATC 2594
Db 4773 CCTCAACAGAGCAATC 4789

RESULT 6
AX653280
LOCUS
DEFINITION AX653280 5760 bp DNA linear PAT 22-MAR-2003
ACCESSION AX653280
VERSION AX653280.1 GI:29156094
KEYWORDS
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,
Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, F. and Zou, G.
Plant genes involved in defense against pathogens
Patent: WO 0300098-A 3150 03-JAN-2003;
Syngenta Participations AG (CH)

FEATURES
Location/Qualifiers
source 1..5760
/organism="Oryza sativa"
/mol_type="unassigned DNA"
/db_xref="taxon:4530"

ORIGIN
Query Match 65.6%; Score 1703.8; DB 6; Length 5760;
Best Local Similarity 79.2%; Pred. No. 0;
Matches 2054; Conservative 0; Mismatches 497; Indels 42; Gaps 1;

QY 1 AGCTTGTGTAAGAAAAATTTATCGCTGGGAAACAAGTTGTTTACTTTATCCAGATGTTTGA 60
Db 2648 AACTTGCTGACCAAGATTGTTCAATGGGTAAACAAGCTTTTCGTTTTCAGAGGCAATGA 2707
QY 61 AAGCTGATTCACAAATGATCTCTATTTCAATCGTGATCTATCAGCTGTGGCCAAATGAGC 120
Db 2708 AGGCTAATTCGACAAATGATGATATTTGAATCGTAAACCTATCGGCTTTGGGCAATGAGC 2767
QY 121 CTGATGCTACTTATCAAGGAGCATTCATGCGGTGGAAGTGGAGATTTTTCACGTGAAAT 180
Db 2768 CTGATGCTCAATCAAGGAGCATTCATGATTTGAGATGGAGGCTTTTCACGAAAGAC 2827
QY 181 TGCACAAGAGAGCTGGCAGGGGACTGGTGGTGTGCTGCAAACTATACATCTCCTAAGCAGG 240
Db 2828 TGCACAAGAGTGAATGATGAGTGGGATTTGGTGTCTTGCAAACTGACATACCAAGGAG 2887
QY 241 CATACAGATGACCTTTGTTTATTAAGGACACACCGTATATGAAATATATACATA 300
Db 2888 CTTATAGATTAGACTTTGTTTCTTCAATGGTTCGTTTATCTATGATACAAATGATAGTA 2947
QY 301 ATGATTTCTGTGATCAAAATAGAAAGCAGCATCGATGAAATTTATTTGAGGATTTCTTGG 360
Db 2948 ATGATTTTGTGCTGCAAGTAGAAGTACATGATGATGAAGATTTCTTTGAGGAGTTCTTGG 3007
QY 361 CTGAAGAAAGCAACGAGAACTTGAGAACTTGCAAATGAGGAAGCTGAAAGGAGAGAC 420

QY 2581 TGAACAGGCGCAT 2593
 |||||
 Db 5186 TGAACAGGCAAT 5198
 |||||
 RESULT 7
 AK122098
 LOCUS
 DEFINITION
 Oriza sativa (japonica cultivar-group) cDNA clone:J033125F11, full insert sequence.
 ACCESSION
 AK122098
 VERSION
 FLI_CDNA; CAP trapper.
 KEYWORDS
 Oriza sativa (japonica cultivar-group)
 Oriza sativa (japonica cultivar-group)
 SOURCE
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 ORGANISM
 1
 The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:
 Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Hayashida, K., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group, Ootomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Nakamura, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:
 Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.
 Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
 JOURNAL
 Science 301 (5631), 376-379 (2003)
 MEDLINE
 22752273
 PUBMED
 12869764
 REFERENCE
 2
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakahama, Y., Nakamura, M., Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Ootomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shingawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and Yoshimura, A.
 Collection, mapping, and annotation of 28K full-length cDNA clones from japonica rice
 JOURNAL
 3 (bases 1 to 4241)
 REFERENCE
 Kikuchi, S.
 Direct Submission
 Submitted (31-JAN-2003) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp)

COMMENT
 This clone is one of the 32K full-length cDNA clones from japonica rice.
 URL : http://cdna01.dna.affrc.go.jp/cDNA/
 NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Yamamoto, M., and Nakahama, Y.
 FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.
 Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Iida, Y., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Oota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.
 Location/Qualifiers
 source
 1. 4241
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /db_xref="taxon:39947"
 /clone="J033125F11"
 ORIGIN
 Query Match 63.4%; Score 1647.2; DB 8; Length 4241;
 Best Local Similarity 77.2%; Pred. No. 0;
 Matches 2003; Conservative 0; Mismatches 593; Indels 0; Gaps 0;
 QY 1 AGCTTGCTGAAATAATATTTCGCTGGGAAACAAGCTGTTTACTTATCCAGATGATTGA 60
 Db 1017 AGCTTGCTGAGAAATAATATTTCGCTGGGAAACAAGCTGTTTACTTATCCAGATGATTGA 1076
 QY 61 AAGCTGATTCACAAATTCATCTCTATTTTCATCGTGATCTATCAGCTGGGCCAATGAGC 120
 Db 1077 AGGCGGATTCGGTCAATTCATCTTACTTGAACCATAGCATGTGAGCCTTAGCCAGTGC 1136
 QY 121 CTGATGTTACTTATCAAGAGGAGCATTCAATGGTGGGAAGTGGAGATTTTCTCTGAAATAT 180
 Db 1137 CTGATTTCTTATCAAGAGGAGCATTCAATGGTGGGAAGTGGAGATTTTCTCTGAAATAT 1196
 QY 181 TGCACAAAGCAGCTGGCAGGAGCTGGTGGTGTGCAAACTATACATTCCTAAGCAGG 240
 Db 1197 TGCATAAAGTGAAGTGAACAGGAGTGGTGGTGTGCAAACTATACATTCCTAAGCAGG 1256
 QY 241 CATACAGAAATGCACTTTGTGTTTTTAAACGACACACCGGTATATGAATAATAATACATA 300
 Db 1257 CTTACAGATTAGATTTCGTTTATTTTAAATGGTGACACCATCTACGAAATAACAATCATA 1316
 QY 301 ATGATTTGTTGATACAAATAGAACCAACCTGGATGAAATTTTATTCAGGATTTCTTGG 360
 Db 1317 ATGATTTGTTGATACAAATAGAACCAACCTGGATGAAATTTTATTCAGGATTTCTTGG 1376
 QY 361 CTGAAGAAAGCAACGAGAACTTGAAGACCTTGCAAATGAGGAAGCTGAAAGGAGAGAC 420
 Db 1377 TTGAAGAAAGCAACGAGAGCTTGAAGGCTTGTCTGCAGAGAGCTGAAAGGAGAGAC 1436
 QY 421 AAACCTGATGAGCAGCGCGGAATGGAGGAAGAAAGGCGCCAGATTAAGCTGACGGGTAC 480

Tel:81-29-838-7007, Fax:81-29-838-7007)

Db 1437 AGGCTGAGGAGCGCTCGTAAGGAGGAAGAAAGGGCTGCAATGGAGGCTGACAGGGCAC 1496
QY 481 AAGCCAAAGCTTGAGGTAGAGACGAAGAAGATAAATGTGCAATGTATTTGGGTTTAGCCA 540
Db 1497 AAGCAAGGCTGAAGTCGAGATGAACAGAATAAGTTGCAAAATTTATTTAAATTCAGCCA 1556
QY 541 GAGCTCCTGTGTATATTTATGTGATCATTTGAGGCCATCAAGCTGACAGAGGCTACTG 600
Db 1557 GCAGATATGCTGATATCTATGTATATAGAGCTCACACATACAAAGCAGGGATAGG 1616
QY 601 TCGAGTTGTATTAACATAAATCAAGACCTTAGTTACAGTACTGAGATATGATGC 660
Db 1617 TCAAAATTTGTTTCAACAAGAGCTCAAGACCGCTAATGCAATACACTGAGATTTGGATGC 1676
QY 661 ATGGTGGCTATTAACAATTTGATGGAGCTCTCTTTTCTGCTGAAGGCTTTTCATCATC 720
Db 1677 ATGGCGGTTTACAATAATTTGAGATGAGGCTCTCTATTTCTGAAAATTAATCAAAATAT 1736
QY 721 ATGACAAAGATTTGATTTGGTTGGTTGCAAGATTTGTCTGTGCTGAAAACATATGTAT 780
Db 1737 ATGAAAAGGATGGTGAATGGTATGAGATGTTTACTCTACTGAAGGGCAATGGTGT 1796
QY 781 TGGACTGGGTTTTGCTGACGGCCACACAGGAGTCCAAAGATTAATGACAAATGGAG 840
Db 1797 TAGACTGGGTTTTTGTGTATGGGCCACCTGGGAATGCAAGGAATTAATGATAACAATGGAC 1856
QY 841 GACATGATTTTTCATGCTACCTTCCAAATAACATGACTCAGGAAGATTAATGGATGGAG 900
Db 1857 GCCAGATTTCCATGCTGTGTTTCCAAATTAATATCTGAGACCTGTTTTGGGTGGAAG 1916
QY 901 AAGAACAAAGGATTTCTATAAAGCTTCAACAAGAGAGGAGGAAGGGAGGCTATTATTA 960
Db 1917 AAGAGCACATGATATTTAAAGGCTTCAGAAAGAAAGAAAGAGGAGGATGCTGATC 1976
QY 961 AAGGAAGCTCGAGAAATGCAAAATCAAAAGCTGAGATGAAGAAAGACTATGAGAA 1020
Db 1977 GAAGAAGTCTGAGATACTGCAAAATGAAGCTGAGATGAAGGAAGAAAGACTATGAGAG 2036
QY 1021 TGTTCCTGTTTTCTCAGAAACACATTTGTTTACACGAACCACTTGAATACATGCTGGAA 1080
Db 2037 ACTTTCTCTCGCAGAAACACATTTGTTTCACTGAGGCTCTCGAATGACGTGAGGAA 2096
QY 1081 CTACTATTGATGCTTTAATATCCCTTCAAPACAGTTCTTAATCGAAAGCCAGAGTTT 1140
Db 2097 CCACCGTGGATTTCTTATACAAATCCGCTTAAACACCGTGTGAACGAAAGCCAGAGTTT 2156
QY 1141 GGTTCGATGTTCTTTAATCGTTGATGATATCCAGGTGGGTTGTGCCAATCAGNAGA 1200
Db 2157 GGTTCAGATGTTCTTTAATCGTTGGACTCATCCCAAGTGGTCTTTGGCCGCCACAGAAGA 2216
QY 1201 TGGTACAAGCAGAAATGGTTCCACACCTTAAAGCAACAGTTTACGTTCCACGAGATGCT 1260
Db 2217 TGGTGAATCGCGAGAATGGTTCCACACTTAAGAGCAACAGTTAGGGTTCTTTGGATGCAT 2276
QY 1261 ATATGATGACTTTGTTTTCTCGAGTCAAGAGAGGTGGAAATTTATAGNATAACAGAAATG 1320
Db 2277 ATATGATGACTTTGTTTTCTCGAGTCGGAAGAAGGTGGAAATATATGACAAACAGGAATG 2336
QY 1321 GGTTAGACTATCATATTTCTGTTTTTGGTCAATTTGCAAGGAACCACTATGACATG 1380
Db 2337 GCATGACTATCATAGTCTCTGACTGATTCGTTGCAAAAGAACCTCTCATGCAATATG 2396
QY 1381 TCCATGCTGTTGAGATGGCAACCAATCGAAAGTTGGAGTCTTTGGTGTATTTGTCA 1440
Db 2397 TGCATATGCAATGAGAAATGGCTCTTATTTGCAAGGTTGGGGGTTCTTGTGATTTGTA 2456
QY 1441 CTAGTCTTTTCAAGTGTGCAAGATTTAGGACAAATGTGAGGTTATTTCTCCAAAGT 1500
Db 2457 CAAAGTCTTTTCAAGGCGGTTCAAGATTTAGGCAACAATGTTGAGGTTATTTCTCAAGT 2516
QY 1501 ACGGTTGCTTGAATCTAAGCAATGTCAGAAATCTCAAAATCCATCAGAGTTTCTTGGG 1560
Db 2517 ATGACTGTTTAAACCTAAGCAATGTGAAGATTTACATTTACCGTCAAAATTTTACTTGGG 2576

QY 1561 GTGGTTCTGAAATAAATGTGTGGCGCTGACTAGTCCGAAGGCCCTTTGTGTTTACTTCTCTGG 1620
Db 2577 GTAATACAGAGATAAAGTATGGTTTGGAAAAAGTTGAAGACGCTCCCTGTCTTACTTCTTGG 2636
QY 1621 AACCTCAAAAATGGGATGTTTGGAGTCGGATATGATATGGCAGGAGCGATGACCGCGAT 1680
Db 2637 AACCAACAGATGGGATGTTTGGGTGGATGTGTCTATGGAAGAAATGACGAGAGTAGAT 2696
QY 1681 TTGGCTTCTTGTCTGCTCTGTCTAGAGTTTCTCTCCAAAGTGGATCTTCTCCGAACA 1740
Db 2697 TTGGCTTCTTCTGCCATCTGCTCTAGAGTTTCTCCGCCAAATGATCTTCTCTCTGATA 2756
QY 1741 TAATACATGCCATGATTTGGTCAAGTCTCCTGTTTCCCTGGCTACACAAGGAAATCTAGC 1800
Db 2757 TTATACATTTGTCATGATTTGGTCAAGTCTCCAGTTGCTTGGCTATTCTAAGGAACAATATG 2816
QY 1801 CCAAGCTAGCTTGGCAAAACGACCGGTGGTATTCCCATCCACAATCTTGAATTTGGAG 1860
Db 2817 CTCAAAATGGACTGTCAATGGCGGGTTGTATTTACCATCCACAACCTTGAATTTGGT 2876
QY 1861 GGCATCATATTTGGCAAAAGCAATGAGATATTTGTATAAAGCAACAACCTGCTCTAATCAT 1920
Db 2877 CACATCATATCGGCAAAAGCAATGSCACGTGTGTATAGGCTACAACTGTTTCATATACGT 2936
QY 1921 ATTCAAAAGGAAGTGTCAAGTCAATGCTGATGCTTCTCTCATCTTTGGGAATTTCTATGGCA 1980
Db 2937 ATTCAAGGGAAGTGTCAAGACATGCTGCTATTGGCCCTCACTTTTCCAAATTTCCAGGTA 2996
QY 1981 TTCTCAATGGAAATGATCCGGATATATGGGATCCGTAACAATGACAACTTTATCCCGGTCC 2040
Db 2997 TTCTGAACGGAATTTGATCCAGATATTTGGGATCCATACAGTGACAAATTTATTCGGTCC 3056
QY 2041 ACTACACTTTGAGAAATGTGTTGAAGGCAAGAGGGCTGCTTAAGAGGCACTGCAAGAGA 2100
Db 3057 ACTATACCTCTGAGAATGTTTGTGAGGGCAAGAGTGTCTGCCAAAAGGCAATGCAACAGA 3116
QY 2101 AGTTTGGGTTACAGCAATCGATGTCCTCCGTCGTAAGGAATGCTCACTGCTCCCTGACAGCC 2160
Db 3117 GCTTTGGACTACAGCAAACTGATACCCCTGTTGTTGGAATTTATCAGTCTGCTGACAGTCC 3176
QY 2161 AAAAGGGATCCACTGATCAAGCATGCGATTCACCGTACACTCGAAAGCAAGCAGCAGG 2220
Db 3177 AGAAGGGAATTCACCTTATCAACATGCAATTTATCGAATCTTTGAACGCAATGGCAGG 3236
QY 2221 TGGTTTTCCTGTTTCAGGCGGCACTCTCGAATCCAAAGTGAATTTGTCAACCTGGGGA 2280
Db 3237 TGGTTTTACTAGGCTCAGCTCCAGATCATCGCATCAAAAGGTGACTTTTACCACTTAGCTA 3296
QY 2281 ATACGCTCCACGGCGTAAACCATGGGCAAGTGAGGCTTTTCCCTTGACCTTACGACGAGCCTC 2340
Db 3297 GTAACTGCAATGGCAATACCATGGTGTGTAAAGCTTTGTTTAACTTATGATGAGCCAC 3356
QY 2341 TCTCGCATCTGATATACGCTGGCTCTGACTTTCACTTCTGGTCCCATCTATATTTGAGCCTT 2400
Db 3357 TATCTCATTTGATTTATGCTGGTGGCGACTTCATCTTGTTCCTTCCATGTTTGAACCTT 3416
QY 2401 CGGCGCTAACCTCAGCTCGTCCCATGCGTATGGAACCATCCGATTTGTCGCAAGACTG 2460
Db 3417 GTGGTTTTAACCCAGCTTACTGCTATGCGTTATGATCTATCCCAATAGTTCCGGAACCTG 3476
QY 2461 GAGGCTCTTTCGACACTGCTCTTCGATGTGGCAATGACAAAGGAAGGAGCCGAGATCCAG 2520
Db 3477 GAGGCTTTTATGACACCGTTTTCGCTGCAAGATGATAGGATCGAGCTCGAGAACGAG 3536
QY 2521 GCTTTGAGCCCAAAGGGTTTGTAGTCTTTCGAGGCTGATGACAAAGGTTTGTACTACGCGC 2580
Db 3537 GCTTTGAGCCCAAAGGGTTTGTAGTCTTTCGAAAGGAGTGTGACAGCAACGGTGTGATTAAGGCC 3596
QY 2581 TGAACAGGGCGATCTC 2596
Db 3597 TTGACAGAGCGATCAC 3612

RESULT 8
AX654187 LOCUS AX654187 3645 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 4057 from Patent WO03000898.
ACCESSION AX654187
VERSION AX654187.1 GI:29157001
KEYWORDS
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
1 Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M., Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, R. and Zou, G.
Plant genes involved in defense against pathogens
Patent: WO 0300898-A 4057 03-JAN-2003;
Syngenta Participations AG (CH)

FEATURES
source
1..3645
/organism="Oryza sativa"
/mol_type="unassigned DNA"
/db_xref="taxon:4530"

ORIGIN
Query Match 63.4%; Score 1646.8; DB 6; Length 3645;
Best Local Similarity 77.1%; Pred.No. 0; Mismatches 593; Indels 0; Gaps 0;
Matches 2002; Conservative 1;

QY 1 AGCTTGCTGAAAAAATATTGCTGCGGAAACAAAGTGTGTTACTTATCCAGATGTATTGA 60
DB 926 AGCTTGCTGAAAAAATATTGCTGCGGAAATAGTGTGTTGTTTCTGGAAGTAGTAC 985
QY 61 AAGCTGATTCAACAATGTATCTTATTTCAATCGTGATCTATCAGCTGTGGCCATGAGC 120
DB 986 AGCGGGAATTCGGTCAATGATCTTTACTTGAACCATAGCATGTGAGCCTTAGCCAGTGAGC 1045
QY 121 CTGATCTACTTCAAGAGCATTCATCAATGGGTGGAGTGGAGATTTTCACTGAAATAT 180
DB 1046 CTGATATCTTATCAAGGGGCAATTCATGTTGGAGATGGAAAAATTTACCCAAAAA 1105
QY 181 TGCACAAGAGCGAGCTGGCAGGGGACTGTGTGCTGCAAACTATACATTCCTTAAGCAG 240
DB 1106 TGCATAAAAGTGAGTTAAACAGGGGATTGTGTGCTGCAAACTCCATATACCCAGCAG 1165
QY 241 CATACAGATGACATTTGTGTTTTTAAACGACACACGGTATATGAAATATAACAATA 300
DB 1166 CTACAGATTAGATTTGTATTCTTTTAAATGGTGACACCATCTACGAAAAATAACAATCATA 1225
QY 301 ATGATTTGCTGATACAAATAGAAAGCACCATGATGAAATTTATTTGAGGATTTCTTGG 360
DB 1226 ATGATTTGCTCTCAAAATAGAAAGCGAATCAATGAACTCAATTTGAGGACTTCTTGG 1285
QY 361 CTGAAGAAAGCAACGAGAACTTTGAGAACTTTGAGAACTGAGAGCTGAAAGGAGAGAC 420
DB 1286 TTGAAGAAAAACAAGAGAGCTTTGAAGGCTTCTGCAAGAAAGCTGAAAGGAAAGAC 1345
QY 421 AAATCTATGAGCGCGGATGAGGAGAGAAAGGCGCGCAGATAAGCTGACAGGGTAC 480
DB 1346 AGGCTGAGGAGGAGCGCTCTAAGAGAGAGAAAGGCTGCAATTTGAGGCTGACAGGGCAC 1405
QY 481 AAGCCAAAGGTTGAGGTAGAGCAAGAAAGAAATAAATTTGTGCAATGTATTGGGTTAGCCA 540
DB 1406 AAGCAAAAGGCTGAAGTCGAGATGAACAGAAATGAATTTGCAAAATTTATTAATTCAGCCA 1465
QY 541 GAGCTCCTGTGTAATTTATGTTATGATCATTTGAGCCCATCAGCTGACGAGAGGCTACTG 600
DB 1466 GCAGATATGCTGATAATCTATGCTATATAGAGCTCAGACATACAAAGCAGGGGATAGG 1525
QY 601 TCGATTTGTTATTAACATTAACCTCAAGACCTCTAGTTTCAAGTACTGAGATATGATGC 660
DB 1526 TCAAATTTGTTCTAACAGAGAGCTCAAGACCGCTAATGTCATAACACTGAGATTGGATGC 1585

QY 661 ATGGTGGCTATAACAATGGATTGATGAGCTCTCTTTTGTGCTGAAAGGCTTGTTCATC 720
DB 1586 ATGGCGGTTACATTAATTTGGAGTGATGGCTCTCTATTGCTGAAAAATTAATCAATCAT 1645
QY 721 ATGACAAAAGATGTGATTTGGTGGTTTGCAGATGTTGTGCTGCTGCTGAAAGAAATATGTAT 780
DB 1646 ATGAAAAGGATGGTGGTGGTATGAGATGTTTACTCTCTGCTGAAAGGCGATTTGGTGT 1705
QY 781 TGGACTGGGTTTTTCTGCTGACGCCCAACAGGAGTGCAAGGAATATATGACAAATGGAG 840
DB 1706 TAGACTGGGTTTTTCTGCTGATGGGCCCTCGGAATGCAAGGAATATATGATAACAATGGAC 1765
QY 841 GACATGATTTTTCATGCTACCCCTTCCAAATAAATGAGTCTGAGGAAGATATTGATGGAAG 900
DB 1766 GCAGGATTTTCATGCTGTTGTTTCCAAATAAATATCTGAGGACCTGTTTTGGTGGAG 1825
QY 901 AAGAAACAAAGGATCTATACAGGCTTCAACAAGAGAGGAGGAAAGGAGGAGGCTTATTA 960
DB 1826 AAGAGCACATGATATTTTAAAGGCTTCAGAAAGAAAGAAAGAAAGGAGGATGCTGATC 1885
QY 961 AAAGGAAGCTGAGAGAAATGCAAAAATGAAAGCTGAGATGAGGAAGAAAGCTATCAGAA 1020
DB 1886 GAAGAAGTCTGAGATACTGCAAAAATGAAAGCTGAGATGAGGAAGAAAGCTATCAGAG 1945
QY 1021 TGTTCCTGGTTTTCTCAGAAACACATTTGTTTACACCGAACCACTTGAAATACATGCTGGAA 1080
DB 1946 ACTTTCTTCTCGCAAGAACACATTTGTGTAACACTGAGCCTCTCGAAGTACGTCAGGAA 2005
QY 1081 CPACTATTGATGTGCTTTATAATCTCTTAATFACAGTTCTAACTGGAAGCCAGCAGAGTTT 1140
DB 2006 CCACCGTGGATGTTCTATACAAATCCGCTTAACACCGTGTGAAACGGAAGCCAGAGGTTT 2065
QY 1141 GGTTCGATGTTTCCCTTAATCGTGGATGTAATCCAGGTGGGTGTTGCCACCTCAGAA 1200
DB 2066 GGTTCGATGTTTCCCTTAATCGTGGACTCATCCAGTGGTCTTTTGGCCGACAGAA 1255
QY 1201 TGGTCAACAGCAAAATGGTTCAACCTAAAGCAACAGTTTACGTTCCACGAGATGCCT 1260
DB 2126 TGGTGAATGCGGAGATGTTTCACTTAAGAGCAACAGTTAGGTTCTTTGGATGCA 2185
QY 1261 ATATGATGACATTCGTTTCTCGGAGTCAGAAAGGTTGAAATTTATGATAACAGAAATG 1320
DB 2186 ATATGATGACATTCGTTTCTCGAGTCGAAAGGTTGAAATATATGACAAACAGGAATG 2245
QY 1321 GGTGATGATCATATTCCTGTTTGGTCAATTCGAAAGGAACCACTATSCACATG 1380
DB 2246 GATGACTATCATAGTCTCTGATGATTCGTTGCAAAAGAACCTCTATGCAATTTG 2305
QY 1381 TCCACATTCCTGTTGAGATGGCAACCAATCGAAAGGTTGGAGTCTTGGTGTGTTGTCA 1440
DB 2306 TGCACATTCGAGTAGAATGGCTCTTATTGCAAGGTTGGGGTCTTGGTGTGTTGTA 2365
QY 1441 CTAGTCTTTCAAGTGTGCAAGATTTAGGACACAATGTGGAGGTTATCTTTCAAAGT 1500
DB 2366 CAAGTCTTTCAAGGAGCGGTTCAAGATTTAGGCCACAATGTGAGGTTATCTTTCCCAAGT 2425
QY 1501 ACGGTTGCTTGAATCTAAGCAATGTCAAGAACTCAAAATCCATCAGAGCTTTTCTTGG 1560
DB 2426 ATGACTGTTTAAACCTTAAGCAATGTGAAAGATTTTACATTTACCGTCAAGATTTTACTTGG 2485
QY 1561 GTGGTTTCTGAAATAAATGTGCGGCTGGAGTCTAGTCTGAAAGGCTTTGTGTTTACTTCTGG 1620
DB 2486 GTAAATACAGATATAAGTATGTTTGGAAAGTTGAAGCGTCCCTGTTTACTTCTGG 2545
QY 1621 AACCTCAAAATGGGATGTTTGGAGTCGGATATGTATATGGCAGGAGCAGATGACCGCGAT 1680
DB 2546 AACCAAGAAATGGGATGTTTGGGTTGGATGTCTATGGAAGAAATGACGAGAGTAGAT 2605
QY 1681 TTGGCTTCTTCTGCTGCTCTAGAGTTTCTCTCCAAAGTGGATCTTCTCCGAA 1740
DB 2606 TTGGCTTCTTCTGCCATCTCTCTAGAGTTTCTCGCCAAATGGATCTTCTCTCTGATA 2665

QY 1741 TAATACATTGGCATGATTGGTCAAGTGTCTCTGTGCTGCTACACAAAGGAAACTACG 1800
Db |||||
2666 TTATACATTGTTCATGTTGGTCAAGTGTCTCTGTGCTGCTACACAAAGGAAACTACG 2725
QY 1801 CGAAGTCTAGCTTGGCAACGACGCGGGTGTATTCACCATCCACAACTTGAATTTGGAG 1860
Db |||||
2726 CTCAAAATGGAGCTGTCAAAATGGCGGGTGTATTTACCATCCACAACTTGAATTTGGT 2785
QY 1861 CGCATCATATTGGCAAGCAATGAGATATGATGATGATGATGATGATGATGATGATGAT 1920
Db |||||
2786 CACATCACATCGCAAGCAATGAGATATGATGATGATGATGATGATGATGATGATGAT 2845
QY 1921 ATTCAAGGAAAGTGTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1980
Db |||||
2846 ATTCAAGGAAAGTGTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATG 2905
QY 1981 TTCTCAATGGAAATGATCGGATATATGGATCGGTACAAATGAACTTATCCGGTCC 2040
Db |||||
2906 TTCGTAACGGAATGATCCAGATATTTGGGATCCATACAGTGACAAATTTATCCGGTCC 2965
QY 2041 ACTACACTGTGAGAAATGTTGAGGCAAGAGGGCTGTAAGAGGCACTGACAGCAGA 2100
Db |||||
2966 ACTATACCTCTGAGAAATGTTGAGGCAAGAGGCTGTAAGAGGCACTGACAGCAGA 3025
QY 2101 AGTTTGGGTTACAGCAAAATGATGTTCCCGTGTAGGAAATCGTCACTCCCTGACAGCCC 2160
Db |||||
3026 GCGTTGGACTACAGCAAAATGATACCCCTGTTGTTGGAATTTATCACTGCTGACAGTCC 3085
QY 2161 AAAAGGGGATCCACTGATCAGATGATGATGATGATGATGATGATGATGATGATGAT 2220
Db |||||
3086 AGAAGGGAATTCACCTTATCAAAATGCAATTTATCGAACTCTTGAAGCAATGGGCAAG 3145
QY 2221 TGGTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2280
Db |||||
3146 TGGTTTCTAGGCTCAGCTCCAGATCATCGATACAGAGTGACTTTACCAACTTAGCTA 3205
QY 2281 ATAGCTCCAGCGGTAAACCAATGGGCAAGTGAAGCTTCCCTGACCTACAGAGCCTC 2340
Db |||||
3206 GTAAACTGCTAGCGGCAATACCAATGGTCTGTGTAAGACTTTGTTAACTTATGATGAGCC 3265
QY 2341 TCTCGCATCTGATACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400
Db |||||
3266 TATCTCATTTGATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3325
QY 2401 GCGGCTTAACCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
Db |||||
3326 GTGGTTTAAACCACTTACTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3385
QY 2461 GAGGCTCTTCGACACTGCTTTCGATGTTGACATGACAAAGGACGAGCCCGAGATCGAG 2520
Db |||||
3386 GAGGCTCTTATGACACCGCTTTTGAACGCTGATGATGATGATGATGATGATGATGATGAT 3445
QY 2521 GCCTTTGAGCCCAACGGGTTTATGCTTTGAGGAGCTGATGACAAAGGCTGCTGCTGCTGCT 2580
Db |||||
3446 GTCTTTGAGCCCAACGGGTTTCACTTTGAGGAGGCTGACAGCAACGGTGTGATACGCC 3505
QY 2581 TGAACAGGCGGATCTC 2596
Db |||||
3506 TTGACAGAGCGATCAC 3521

RESULT 9
AX755430
LOCUS AX755430 3032 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 131 from Patent WO03000905.
ACCESSION AX755430
VERSION AX755430.1 GI:32167798
KEYWORDS
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1
AUTHORS Zhu, T., Cheng, W., Briggs, S., Cooper, B., Goff, S.A., Moughamer, T., Glazebrook, J., Katagiri, F., Kreps, J., Provart, N. and Rieke, D.
TITLE Identification and characterization of plant genes
JOURNAL Patent: WO 03000905-A 131 03-JAN-2003;
Syngenta Participations AG (CH)
FEATURES
Location/Qualifiers
source 1..3032
/organism="Oryza sativa"
/mol_type="unassigned DNA"
/db_xref="taxon:4530"
ORIGIN
Query Match 60.9%; Score 1581.4; DB 6; Length 3032;
Best Local Similarity 77.5%; Pred. No. 0;
Matches 2048; Conservative 0; Mismatches 491; Indels 102; Gaps 7;
QY 1 AGCTTGCTGAAAAAATTTTCGCTGGGAAACAAGTTGTTTACTTATCCAGATGTATTGA 60
Db |||||
323 AACCTGCTGACCAAGATTTTCAATGGGTAACAAGCTTTCGTTTCCAGAGCGAGTGA 382
QY 61 AAGCTGATTCAACAATGATCTCTATTTCATCGTGAATCTACAGCTGTGSCCAATGAGC 120
Db |||||
383 AGGCTAATTCGACAAATGATGATATTTGAATCGTAACCTATCGCTTTGCGGATGAGC 442
QY 121 CTGATGCTATTCACAAAGGAGCATTCAATGGGTGGAAGTGAGATTTTTCAGTGAATAAT 180
Db |||||
443 CTGATGCTTCCATCCAAAGGAGCATTCAATGTTGAGATGAGGCTTTTCCAGGAAGAC 502
QY 181 TGCACAGAGAGCTGCGAGGGGACTGGTGGTCTGCAACTATATCATCTTCTTAAGCAGG 240
Db |||||
503 TGCACAGAGAGTGAATTCAGTGGGATTTGGTCTTCCAACTGCACATACCCAGGAAG 562
QY 241 CATACAGATGAGCTTTGTTTAAACGACACACAGTATATGAAATTAATACATA 300
Db |||||
563 CTTATAGATTAGACTTTGTTCTTCAATGGTCTGTTAGTCTATGATAACAATATAGTA 622
QY 301 ATGATTTTCGTGATACAAATAGAAAGCACCATGGATGAAATTTTATTTGAGATTTCTTGG 360
Db |||||
623 ATGATTTTCGTGCAATGAAAGTACATGATGATGATGATGATGATGATGATGATGATGAT 682
QY 361 CTGAAGAAAAGCAACGAGAACTTTGAGAACCTTGCAAATGAGGAAGCTGAAAGGAGGAGAC 420
Db |||||
683 TTGAAGAAAAGAAAAGAACTTTGAGAGAGTTGCACTGAAAGAGCTGAAAGGAGGAGGC 742
QY 421 AAACCTGATGAGCAGCGGAGTGAAGAAAGGCGCGAGATAAGCTGACAGGCTAC 480
Db |||||
743 ATGCTGAAGAGCAGCAGGAATGGAGAACAAAGGGCTGAGAACAAAGCTGCCAGGGAAC 802
QY 481 AAGCAAAGTTGAGGTGAGACGAAAGAAATAAATTTGTCATGATTTGGGTTTAGCCA 540
Db |||||
803 AGGCTAAGAGGAGATAGAGTTGAGAAAGAACAAATTTGCAAAATCTGTTGAGTTCAGCCA 862
QY 541 GAGCTCTGTTGATATTTATGTTGTTGAGGCTGAGTCTTATTTGTTGAAAGACTTGTGCAATG 600
Db |||||
863 GAACACATGTTGTAATTTGTCGACATAGAGCTTACATATAGACAAAGGAGGACACTG 922
QY 601 TCAGATGTTATTAACATAAACTCAAGACTCTGTTTACAGTACAGTACAGTACAGTACAGTAC 660
Db |||||
923 TCAGATGTTACTATTAACAGAACTCAAGGCGCTTATGCTAGTACTGAGATCTGAGATG 982
QY 661 ATGGTGGCTATAACAATTTGATGAGTCTCTTTTGTCTGAAAGCTTGTTCATCATC 720
Db |||||
983 ATGGTGGTTCATATGTTGAGTCTGAGTCTCTTATTTGTTGAAAGACTTGTGCAATG 1042
QY 721 ATGACAAAGATTGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 780
Db |||||
1043 ATGACGAAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1094
QY 781 TGGACTGGGTTTTTGTCTGAGCGGCCACCGAGGAGTGCAGGAATTTATGACAAATGAG 840
Db |||||
1095 TGGACTGGGTTTTTGTCTGAGCGGCCACCGAGGAGTGCAGGAATTTATGACAAATGAG 1154

```
QY 841 GACATGATTTTCATGCTAGCCCTCCAAATAAACAATGACTGAGGAAGAGTATTGGATGAAG 900
Db 1155 GACAAGATTTTCATGCTATTCTTCORATGCCATGACTACGAGAAATATTGGTTGAAG 1214
QY 901 AGAAACAAAGGATCTATACAGGCTTCAACAGAGAGGAGGAAAGGAGGAGCTATTAA 960
Db 1215 AGGAAACATGATCTATACAGGCTTCTCCACGAGATCAGAGAACGGGAGGAGCTATTAA 1274
QY 961 AAAGGAAGGCTGAGAGAAATGCAAAATGAAGCTGAGTGAAGGAAGAAAGACTATAGAA 1020
Db 1275 A-----AATAAGAAATCTGAGATGAAGGAAGAAAGACTATAGAA 1313
QY 1021 TGTTCCTGGTTTCTCGAAACACATTTGTATACACCGAACACATTTGAAATACATCTCGGAA 1080
Db 1314 TGTTTCTACTTCTCAGAAACACATTTGTATATCTGAAACCATTTGAAATACGTTCTGGA 1373
QY 1081 CTAATAATGATGTGCTTATATATCTTCTTAAATCAAGTTCTAAATCAAGTTCTTAAAT 1140
Db 1374 CAACTGTGATGTTCTATATATCTTCTTAAATCAAGTTCTTAAATCAAGTTCTTAAAT 1433
QY 1141 GGTTCGATGTTCTTAAATCAAGTTCTTAAATCAAGTTCTTAAATCAAGTTCTTAAAT 1200
Db 1434 GGTTCGATGTTCTTAAATCAAGTTCTTAAATCAAGTTCTTAAATCAAGTTCTTAAAT 1493
QY 1201 TGSTACAAGCAGAAATGTTTCAACCTTAAAGCAACAGTTTA-CGTTCCACGAGATGCC 1259
Db 1494 TGSTGAAPACAGAAATGTTTCACTTAAAGCGACAGTTAGTTTCCATCGGATGCT 1553
QY 1260 TATATGATGACTTGTGTTTCTCGAGTACAGAAAGGTTGAAATTTATGATTAACAGAAAT 1319
Db 1554 TATATGATGACTTGTGTTTCTCGAGTACAGAAAGGTTGAAATTTATGATTAACAGAAAT 1613
QY 1320 GGTGTAGACTATCATATCTGTTTGGTTCATTTGCAAGGAAACCACTATGCAATT 1379
Db 1614 GGAACAGACTAUCATATCTGTTTCTGTTTCCATGCAAGAGGCTTCCATTCATATT 1673
QY 1380 GTCCACATTTGCTGTTGAGATGGACCAATCGCAAGGTTGGAGGCTTGTGATGTTGTC 1439
Db 1674 GTCCATATAGCGTTGAGATGGACCCATGCAAGGTTGGAGGCTTGTGATGTTGTC 1733
QY 1440 ACTAGTCTTTCAGTGTGCAAGATTTAGGACACAAATGTGAGGTTTATCTTCCAAAG 1499
Db 1734 ACAAGTCTTTCAGTGTGCAAGATTTAGGACACAAATGTGAGGTTTATCTTCCGAAA 1793
QY 1500 TACGGTTGCTTGAATCTAAGCAATGCAAGATCTCAAAATCCATCAGAGTTTCTTGG 1559
Db 1794 TATAATTTATGANTCAAGCAATGCAAGATTTGCAATGCAAGCTTCTTCCATCTTGG 1853
QY 1560 GGTGTTTGAATAAATGTTGCGGTGGAATAGTCAAGGCTTTTGTGTTTACTTCTTG 1619
Db 1854 GGTGTTTGAATAAATGTTGCGGTGGAATAGTCAAGGCTTTTGTGTTTACTTCTTG 1913
QY 1620 GAACCTCAAAATGGATGTTGAGTGGATATGATATATGAGGAGGACGATGACCGGGA 1679
Db 1914 GAACCTCAAAATGG-----GTATATGAGGGAACGATGCTGCGAGA 1954
QY 1680 TTTGGCTTCTTCTGCTGCTGCTAGAGTTTCTCTCCTCAAGTGGATCTTCTCGGAC 1739
Db 1955 TTTGGCTTCTTCTGCTGCTGCTAGAGTTTCTCTCCTCAAGTGGATCTTCTCGGAC 2014
QY 1740 ATAATACATTTGCCATGATTTGCTCAAGTGTCTGTTGCTTGGCTACACAGGAAACTAC 1799
Db 2015 ATAATACATTTGCCATGATTTGCTCAAGTGTCTGTTGCTTGGCTACACAGGAAACTAC 2074
QY 1800 GGAAGTCTAGCTTGGCAACGACGAGTGTGATTCACCATCCAAATCTTGAATTTGA 1859
Db 2075 GCAGATTCAGGTTGGCAACGAGTGTGATTTACCATCCAAATCTTGAATTTGA 2134
QY 1860 GGCATCATATTGGCAAGCAATGAGATTTGTGATAAAGCAACATGCTCTCATATACA 1919
Db 2135 GCACATTTTATGGAAGCAATGACATCTGCGACAAAGCCCAAC-----TAGC 2185
QY 1920 TATTCAAGGAAGTGTACGCTGATGGTCCATAGTTCTCTCATCTTGGGAAATCTATGGC 1979
```

```
Db 2186 TATTCAAGGAAGTCCAGGTCATGGTCCATAGCTCCTCACTCGTGGAAAATCTATGGA 2245
QY 1980 ATTCTCAATGGAAATTTGATCCGATATATGGGATCCGTACAAATGACAACATTTATCCGGTTC 2039
Db 2246 ATTCTCAATGGAAATTTGATCCGATATATGGGATCCATATACTACTGATAACTTCATCCGGTA 2305
QY 2040 CACT-----ACACTTGTGAGA 2056
Db 2306 TAGTCATGATAGTCGAATACATTTTATACAACTACAGTCCATATATACTTCTGAAA 2365
QY 2057 TGTGGTTGAAGCAAGAGGCTCTAAAGAGGCACTGACGAGCAAGATTTGGGTTAGACGA 2116
Db 2366 TGTGGTTGAAGCAAGATGCTGCAAGAGAGCAATTTGACGAGAGTTTGGACTGACGA 2425
QY 2117 AATCGATGTCCTCGTGTAGGAATCGTCACTCGCTTGAAGGCCAAAGGGGATCCACCT 2176
Db 2426 GACTGATGTCCCAATTTGTTGGAATCATCTCGTCTGACAGCCAGAGGGTATCCACCT 2485
QY 2177 GATCAGCATGCGATTCACGCTACACTCGAACGGAACGACAGGTGTTTGGTTCGTTTC 2236
Db 2486 CATTAAACATGCACTTCATCGGACCTTGAACGCAATGACAGGTGTTTGGTTCGTTTC 2545
QY 2237 AGCGCCGCACTCTCGAATCCAAAGCTGATTTTGTCAACCTTGGGGAATACGCTCCACGGCGT 2296
Db 2546 AGCTCCAGATCCTCGGATACAGAGTGAATTTCTGCAGATTGGCTGATAGTCTTCATGCTGA 2605
QY 2297 AAACATGCGCAAGTGAAGGCTTTTCCCTTGACCTACGACGAGCCTCTCTCGACTCTGATA 2356
Db 2606 AAACCATGCGCAGGTTAGACTATGTTTAACTTATGACGAGCCTCTCTCACCTGATATA 2665
QY 2357 CGTGGCTCTGACTTCATTCCTGCTCCATCTATATTTGAGCCTTGGCGCTTAACCTAGCT 2416
Db 2666 TGTGCTGCTGACTTCATTCCTGCTCCATCTATGTTCCATCCATCTTTGAAACCTTGGCTGACTCACT 2725
QY 2417 CGTGGCATGCGGTATGGAACCATCCGATTTGTCGCAAGACTGGAAGG-CTCTTCGACA 2475
Db 2726 TGTGTCATGCGCTATGATCCATCCCTATTGTTGGAATAACGAGGAGACTTTAGACA 2785
QY 2476 CTGCTTTCGATGTTGGAATGACAGGAACGAGCCGCGAGATCGAGCCTTGAAGCCCAAG 2535
Db 2786 CTGCTTTCGAGCTAGACCATGACAGACCGGCTCGAGTCTTAGGCTTGAACCAATG 2845
QY 2536 GGTGTTAGCTTTGACGAGCTGATAGCAACGCTGTTGACTACGCTGGAACAGGCGGATCT 2595
Db 2846 GGTTCAGCTTTGATGAGGCTGACTGTAATGTTGTTGATTAAGCCCTGAAACAGAGCAAT 2905
QY 2596 C 2596
Db 2906 C 2906
```

RESULT 10

```
AR353090
LOCUS AR353090
DEFINITION Sequence 1 from patent US 6590141.
ACCESSION AR353090
VERSION AR353090.1 GI:33758579
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4121)
AUTHORS Froberg, C.
TITLE Nucleic acid molecules from plants encoding enzymes which
participate in starch synthesis
JOURNAL Patent: US 6590141-A 1 08-JUL-2003;
FEATURES
source location/Qualifiers
1..4121
/organism="unknown"
/mol_type="genomic DNA"
```

ORIGIN

Query Match	57.8%;	Score 1500.4;	DB 6;	Length 4121;
Best Local Similarity	74.4%;	Pred. No. 0;	Mismatches 601;	Indels 63; Gaps 1;
Matches 1934;	Conservative 0;			
Qy	1	AGCTTGTGTAAGAAATATTCGCTGGGAACAAAGTTGTGTTTACCTATCCAGATGATTTGA	60	
Db	1298	AGCTTGTGATGAGAAATATTCGACTGGGAACAACTGTTTGTGTTTCCCTGAAGTAGTA	1357	
Qy	61	AAGCTGATTCACAAATGATCTCTATTTCAATCGTGATCTATCAGCTGTGGCCCAATGAGC	120	
Db	1358	AGGCTGATTCGATGATGATCTTTTACTTAAACCCGACGATGTCGGCCCTTAGCTAGTGAGT	1417	
Qy	121	CTGATGTAATTCACAAAGGAGCAATTCATGGGTGGAAGTGAGATTTTTCACCTGAAAAAT	180	
Db	1418	CCGACGTTTTTGTAAAGGAGCAATTCATGGTTGGAGATGGAACCGTTTCACTGAAACAA	1477	
Qy	181	TGCAACAGAGCGAGCTGGCAGGGGACTGGTGGTCTGCAAACTATACATTCCTTAAGCAGG	240	
Db	1478	TGCATAGAAGCGAATTAAGAGGGGATTTGGTGGTCTGCAAGCTCTACATTCCTCAAGCAGG	1537	
Qy	241	CATACAGATGGACTTTGTGTTTAAACGACACACGATATATGAAATTAACATTAACATTA	300	
Db	1538	CATACAGACTAGACTTTGTATTTTAAACGGTGACACTGTCTATGAAATTAACATTAACATTA	1597	
Qy	301	ATGATTTGCTGATACAAATAGAAAGCACCATGGATGAAAAATTTATTTGAGGATTTCTTGG	360	
Db	1598	ACGATTTTCTGGAATAGAAAGTGACATAGATGAACACTCATTTGAGGACTTCTTGG	1657	
Qy	361	CTGAAGAAACGACGAACTTGAGAACCTTGCMAATGAGGAAGCTGAAAGGAGGAGAC	420	
Db	1658	TTGAAGAAACGAAAGAACTCGAGAGGCTTGTGTCAGAGAAGAGCTGAAAGGAAAGAC	1717	
Qy	421	AAACTGTGATGACGCGGCGAATGAGGAAGAAAGGCGCGAGATAAAGCTCACAGGGTAC	480	
Db	1718	AAGCTGAGGACGGCACAGGAGAGAGGAAGAAAGGCGCGCATGGAAGCTGACAGGGCAC	1777	
Qy	481	AAGCCAAAGTTGAGGTAGAGACGAGAAAGAAATAAATTTGTCAAATGTAATTTGGGTTTAGCCA	540	
Db	1778	AAGCAAGTCTGAGGTCCAGATGAAGAAAGAAATTCGGCCAGATGTTGATTTGGGCTA	1837	
Qy	541	GAGCTCTGTTGATTAATTTATGTTGATCATTTAGACCCATCAGACTGGACAGAGGCTACTG	600	
Db	1838	GCAGATATGCTGAGAACTTATGGTACATAGAACCTTAACACCTACAGAGGAGGAGACAG	1897	
Qy	601	TCAGATTTGATTAATAACATAAACTCAAGACTCTAGTTTCAAGTACTGAGATATGGAATGC	660	
Db	1898	TTAGATTGTTACTATTAATAGAGCTCGAGATCACTAATGCAATACACTGAGATTGGATGC	1957	
Qy	661	ATGGTGGCTATAACAAATTTGATTTGAGACTCTCTTTTGTGTAAGAGGCTTGTTCATATC	720	
Db	1958	ATGGAGGTTATAACAACTGGATTGATGGACTCTCAATAGCTGAAAGACTTGTCAAATCTC	2017	
Qy	721	ATGCAAAAGATTGATTTGTTGTTGAGATGTTTCTGCTGCTTCAAGAAACATATGAT	780	
Db	2018	ATGAAAGGAAAGGCGATTGGTGGTATGAGAGTTTACATTTACCTGAAAGGCGATTGGGT	2077	
Qy	781	TGGAATGGGTTTTTCTGACGCGCCACACAGGAGTGCAAGGAATTAATGACAAATGAG	840	
Db	2078	TGGATTGGGTTTTTCTGATGACACCTTGGAAATGCAAGGAATTAATGATAACATGGA	2137	
Qy	841	GACATGATTTTCTACCTTCCAAATTAACATGACTGAGGAAGAGTTTGGATGGAAG	900	
Db	2138	GGCAGGATTTTCTATGCCATGTTCTCTAATAACATATCGGATGATATCTTTTGGTGGAG	2197	
Qy	901	AGAACAAAGGATCTATACAGGCTTCAACAGAGAGGAGGGAAGGGAGGAGCTATTA	960	
Db	2198	AAGAACATAGGATCTTTTCAAGGCTTCAACAGAGAGAGAGAGAGGAGAGTGGCGAAA	2257	
Qy	961	AAAGGAAGGCTCAGAGAAATGCAAAATGAAAGCTGAGATGAAGGAAAGACTATGAGAA	1020	
Db	2258	GAATAAAGGCTGAGAGATCTGCAAAATGAAAGGCTGAGATGAAGGAAGACTATGAGAG	2317	
Qy	1021	TGTTCTGTTTCTCAGAAACACATTTGTTTACCGGAACCACTTGAAATACATGCTGGAA	1080	

Db	2318	CGTTTCTGCTCTCACAAACACATATTTGTGTATCTAGCCACTCGAAGTACGTGCAGAA	2377	
Qy	1081	CTACTATTGATGCTTTTATAATCCCTTCTTAATACAGTTCTAACTGGAAAGCCAGAGTTT	1140	
Db	2378	CCACTGTGGACGCTTCTTTATAATCCCTTCTTAACACAGTGTGAATGGAAAGCTCAGAGGTT	2437	
Qy	1141	GGTTTCGATGCTTCTTAACTCGTTGGATGATCCAGGTGGGTGTTGCCACCTCAGAA	1200	
Db	2438	GGTTTCGAGGTTTCTTTAACCGTTGACTCATCAAGTGTGCTTACCAACACAGAA	2497	
Qy	1201	TGTTTACAGCAGAAATTTGTTTCAACCTAAAGCAACAGTTTACGTTTCCACGAGATCCCT	1260	
Db	2498	TGTTTAAAGGCTGAGATAGTTTCACTTACGAACAACAGTCAGTGTTCCTCTGGATCAT	2557	
Qy	1261	ATATGATGGAATTCGTTTCTCGAGTCAGAAAGTGAATTTATGATAACAGAAATG	1320	
Db	2558	ATATGATGGAATTTGTTTCTCTGAGTCGGAAGGTTGGAAGATATGCAATAGGAACG	2617	
Qy	1321	GGTTTACACTATCATATTCCTGTTTGGTCAATTCGAAAGGAACCACTTATGCACATTTG	1380	
Db	2618	GGATGATTAATCATATTCCTGTGTCTGATTGGTTTGAAGGAACCTTCAATGCATTTG	2677	
Qy	1381	TCCACATTTGCTGTTAGATGGACCAATCGAAAGTTGAGGTCCTTTGGTGAATTTGTCA	1440	
Db	2678	TACACATTTGAGTGAATGGCTCTATCGAAAGTTGGAGGCTTTGGTGAATTTGTTA	2737	
Qy	1441	CTAGTCTTTCACGTCGTGTCAGGATTTAGGACACAAATGTTGGAGTTTATTTCTTCAAGT	1500	
Db	2738	CAAGCTTTTTCACGAGCTGTTTACGATTTTAGCCATTAAGTTGAGGTTTATTTCTGCCAAGT	2797	
Qy	1501	ACGTTTCTGCTTGAATCTAAGCAATGTCAGAAATCTACAAATCCATCAGAGTTTCTTGGG	1560	
Db	2798	ATGATTTTAACTCTAAGCAGTGTGAAGGATTTTACACTCAACAACAAAGTTTCTCTCGG	2857	
Qy	1561	GTGTTCTGTAATAAATGTTGGGCTGGAATGTCGAAAGGCTTTGTGTTTACTTCTCTGG	1620	
Db	2858	GTGCAACAGAGTAAAAAGTATGTTTGGAAAGGTTGAAGATCTGCCAGTTTACTTCTTGG	2917	
Qy	1621	AACCTCAAAATGGGATGTTTGGAGTCGATATGATATGGCAGGAGCATGACCGCGAT	1680	
Db	2918	AACCAAAATGGGATGTTTGGGTTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	2977	
Qy	1681	TTGCTTCTTCTGCTGCTCTAGAGTTTCTCTCCAAAGTGGATCTTCTCCGAACA	1740	
Db	2978	TTGCTTCTTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3037	
Qy	1741	TAATACATTTGCAATGTTGTCAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1800	
Db	3038	TCATACATTTGTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3097	
Qy	1801	CGAAGTCTGAGTTTGGCAAAACGACGGGTGGTATTCACCATCCAAATCTTGAATTTGGAG	1860	
Db	3098	CTCTTAATGGGCTGGGAATGTTGGATTTGTTTACCATCCAAATCTTGAATTTGGAG	3157	
Qy	1861	CGCATCATTTTGGCAAAAGCAATGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1920	
Db	3158	CGCATCATTTTGGCAAAAGCAATGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	3217	
Qy	1921	ATTCAAAGGAAGTGTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1980	
Db	3218	ATTCAAAGGAAGTGTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3277	
Qy	1981	TTCTCAATGGAAATTTGATCCGATATATGGGATTCGTTCAATGCAACATTTTATCCCGTCC	2040	
Db	3278	TTGAAATTTGAAATTTGATCCCTGACATTTGGGATTCATATCTGACAGATTTTATCCGGTTC	3337	
Qy	2041	ACTACACTTGTGAGAAATTTGTTGAGGCAAGAGGGCTGTCTAAGAGGCACTGACGACGA	2100	
Db	3338	ATTATACATCAGAGAAATGTTCTTGGGGCAAGGGTGTCTGCAAAAAAGGCAATTTGACGACA	3397	
Qy	2101	AGTTTGGTTTACAGCAATTCGATGCTCCCGTCTGAGGAATCGTCACTGCTGCTGACGCCC	2160	

YNNWIDGLSIAERLVKSHKEGDDWWYVEVTLPERALVLDWYFADEPGCNGARNYDNNKG
QDFHAIYNNISDDIIFWEEERHETPLRUQQRERRERESAEKRIKAERSAKNKAEMKCTGP
RALISLQKHIVYLEPLEYRAGTVDVNLNPNVNLNGSEKSVYWFNRGSRNWRHPSPGELP
PQWKAENSGLHETTPVLDVADNMDFVSEBEGGYDRNRGNDYHPIPVSDSVARE
PKMHIVTAASHEMATKVGGLDDVNTLSRAVQDILGHKEVILPKYDCLILSSKDLH
YQOSFASGTEYKGVWFGVGLDLPYVFLPQNGMFWGCVYGVKNDSSRGFGFCHSALEF
LILQKSSPDI1CHCDMSAPVAYLVKQYALVGLNGRIVFTLHNLFGAAHIGKAMA
HCDKATVSDTYSKEVAGHALAPHYKFEHGRNGIDPDIDPDYDTRDTPVHYTSENV
LEGGAALKQOMLGLOTHDSPPVGLITRUTVQKGIHLIUKHAMRAERNQCVVILG
SAPDHRIQDNTLASKGHEHYGRVKILTRUTVQKGIHLIUKHAMRGYGSIP1VKTQGLY
DITFVDDDKORQAQGLDEPNGFSFEGADSGVDYALDRAITAFYDARDWFNSLSKRV
MEODWSNRPAIDYMWELVHSARKN"

Query Match	57.8%;	Score 1500.4;	DB 6;	Length 4121;
Best Local Similarity	74.4%;	Pred. No. 0;		
Matches 1934;	Conservative	0;	Mismatches 601;	Indels 63; Gaps 1;
QY	1	AGCTGCTCAAAAAAATATTTCGCTGGGAAAACAAGTTGTTTACTTATCCAGATGTATGCA	60	
Db	1298	AGTTTGTCTGATGAGAAATATTTCGACTGGGAAACAACGTGTTTGTTCCTCGAGTAGTCA	1357	
QY	61	AAAGCTGATTCAACAATTGATCTCTATTTCCAATCGTGATCTACAGCTGTGGCCAATGAGC	120	
Db	1358	AGGCTGATTTCGATGATTGATCTTTTACTTAAACCGCAGCATGTCGGCTTGTAGCTAGT	1417	
QY	121	CTGATGTACTTATCAAAAGAGCAATTCAAATGCGTGGAGTGGAGATTTTTCACGTAAAAAT	180	
Db	1418	CCGACGTTTTTGTAAAGAGGAGATTCAATGGTTGGAGATGGAAACCGTTTCACTGAAACAA	1477	
QY	181	TGCACAAGAGCGAGCTGGCAGGGGACTGTGTGTCTGCAAACTATACATTCCTTAAGCAGG	240	
Db	1478	TGCATAGAAGCAATTAAGAGGGGATTGTGTGTCTGCAAGCTCTACATTCCTCAAGCAGG	1537	
QY	241	CATACAGATGGACATTGTGTTTTTAAACGGACACACGGTATATGAAATATAACAATA	300	
Db	1538	CATACAGACTAGCACTTGTATTCTTTAAACGGTGACACTGCTATGAAAAATAACAATCA	1597	
QY	301	ATGATTTCTGTATACAAATAGAAAGCACCATGGATGAAAAATTTATTTGAGGATTTCTTGG	360	
Db	1598	ACGATTTTTCTGGAAATAGAAAGTGACATAGATGAACACATTCATTGAGGACTTCTTGG	1657	
QY	361	CTGAAGAAAAGCAACGAGAACTWTGAGAACTTTGCAAACTGAGGAAGCTGAAAGAGAGAC	420	
Db	1658	TTGAAGAAAAGCAAGAGAACTCGAGAGCGTTGCTCGAAGAGAGCTGAAAGAAAAGAC	1717	
QY	421	AAACTCATGAGCAGCGCGGAAATGAGAGAAAGAAAGGCGCGCAGATAAGCTGACAGGGTAC	480	
Db	1718	AACTTAGAGCGGCACAGAGNAGAGAAAGGCGCGGATGGAACTGACAGGGCAC	1777	
QY	481	AAAGCCAAAGTTGAGGTAGAGACGAAGAAATAAATTTGCAATGATTGGGTTTAGCCA	540	
Db	1778	AAAGCAAGGTCGAGGTCGAGATGAAGAAAAGAAATGCGCCAGATGTTGAGTTCGGCTA	1837	
QY	541	GAGCTCCTGTGTATTTATTTGTTACATTTGAGCCCATCAGCTGACAGAGAGGCTACTG	600	
Db	1838	GCAGATATGCTGAGAACTTATGGTACATAGACCTAACACCTACAGAGAGGAGACAGAG	1897	
QY	601	TCAGATTGTATTATAACATAAACTCAAGACCTCTAGTTTCACAGTACTGAGATATGGATGC	660	
Db	1898	TTAGATTGTACTATAATAGAAGCTCGAGATCACTAATGCATAACACTGAGATTGGATGC	1957	
QY	661	ATGGTGGCTATAACAATTTGATTTGGACTCTCTTTTGTCTGAAAGGCTTTTCATCATC	720	
Db	1958	ATGAGAGTTTATAACAATCGAATTGATGGACTCTTCAATAGCTGAAAGACCTTGTCAAAATCTC	2017	
QY	721	ATCACAAAAGATTCTGATTTGTGTGTTTTGCGAGUCTTCTGTCGCTGAAAGAAACATATGTAT	780	
Db	2018	ATGAAGAAGNAGCGAATTTGTGTATGTAGAGTTTACATTACCTGAAAGGGCAATTTGGTGT	2077	
QY	781	TGGACTGGGTTTTTGTGACGGCCCCACCGAGGTGCAAGGAATTATGACAAACAATGGAG	840	
Db	2078	TGATTTGGGTTTTTGTGTATGGACCACTTGGGAATGCAAGGAATTTATGATAACAATGGAA	2137	

```

RESULT 11
AX085557          4121 bp      DNA          linear      PAT 09-MAR-2001
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1
Frohberg,C.
Nucleic acid molecules derived from plants which code for enzymes
which are involved in the synthesis of starch
Patent: WO 0112826-A 1 22-FEB-2001;
Aventis CropScience GmbH (DE)
Location/Qualifiers
1..4121
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"
442..3954
/feature="unassigned protein product"
/codon_start=1
/db_xref="GI:13275594"
/translation="MWNMLRAEPLKSGRGPALIVRPAAATGIALSVRCRSFRTGG
LVRCWSSSDYPKPNRRASPSKGVASGYAPRTAESSTKKIQSRNMGDFDRA
NGSLVGBAAEOAATBSSSOVYMTGDIILSGAERDGACTEEADQONQSALPSASMDID
SIDRQLDEYRKILGALVSSKEPSSLASVAGNESVGGFHGQHEPTIGSEHGHSSIVD
APIKRLFAEAVAGWQKDTFSAAGKASNEEGQAVSLEDVGIISDADELPVSSDD
PEVLLRRLQELADENYLTGNRCVFVPEVKADSMIDLYLNRSMSALASSDVFKGAF
NGWNRNFTETMHRSELRGWNCCKLYIPKQAVRLDFVFNFGDTVYNNHNDFFLEI
ESDIDESHFDFPLVSSAEKKEILERAEEARKQAEHRREERERAMEADRAQARSE
UEMKFQVPLVSSAEVAENILVYNNFTVYGGCDVPIVYNNRSRI MHNTFTVMHGCG

```

QY 841 GACATGATTTTCATGCTACCTCCCTTCCAAATTAACATGACTGAGGAAGATATTGGATGAAG 900
Db 2138 GGCAGGATTTTCATGCCATCGTTCTCTAATAACATATCGGATGATATCTTTTGGGTGGAAG 2197
QY 901 AAGAACAAAGGATCTATACAGGCTTCAACAGAGAGAGGGAAGGAGGAGGCTATTGA 960
Db 2198 AAGAACATAGGATCTTTACAGGCTTCAACAGAGAGAGGGAAGGAGGAGTGCAGAA 2257
QY 961 AAAGGAAGGCTGAGAGAAATGCAAAAAATGAAGCTGAGATGAAGGAAGAAAGCATATGAGAA 1020
Db 2258 GAATAGGCTGAGAGATCTGCAAAAATGAAGCTGAGATGAAGGAAGAAAGCATATGAGAG 2317
QY 1021 TGTTCCTGGTTCTCAGAAACACATTTGTTACCGAACCACTTTGAATACATGCTGAA 1080
Db 2318 CGTTTCTGCTCTCAAAAAACATATTTGTATCTAGAGCCACTCGAAGTAGCTGCAGAA 2377
QY 1081 CTACTATTGATGTCTTTATATCTCTTAATACAGTTCTTAATCTGGAAGCCAGAGGTTT 1140
Db 2378 CCATGAGGAGTTCTTTATATCTCTTAATACAGTTCTTAATCTGGAAGCCAGAGGTTT 2437
QY 1141 GGTTCGATGTTCTTTAATCGTTGGATGATACAGGTTGAGTCCAGGTTGGTTCCTCAGAGA 1200
Db 2438 GGTTCAGAGGTTCTTTAATCGTTGGATGATACAGGTTGAGTCCAGGTTGGTTCCTCAGAGA 2497
QY 1201 TGGTACAGAGAAATGGTTTACACCTTAAAGCAACAGTTTACGTTCCAGAGATGCT 1260
Db 2498 TGGTAAAGGCTGAGAAATGTTTACACCTTAAAGCAACAGTTTACGTTCCAGAGATGCT 2557
QY 1261 ATATGATGAGTCTGTTTCTCGAGTCCAGAGAGGTTGGAATTTATGATAACAGAAATG 1320
Db 2558 ATATGATGAGTCTGTTTCTCGAGTCCAGAGAGGTTGGAATTTATGATAACAGAAATG 2617
QY 1321 GGTTAGACTATCAATCTCTGTTTGGGTCATATGCAAAAGAACCACTATGACATG 1380
Db 2618 GGATGATTTATCATATCTCTGTTTGGGTCATATGCAAAAGAACCACTATGACATG 2677
QY 1381 TCCACATGCTGTTGAGATGCAACCAATCGCAAGGTTGGAGGCTTGGTATGTTGCA 1440
Db 2678 TACACATGCGAGTGAATGGTCTCTATCGCAAGGTTGGAGGCTTGGTATGTTGTA 2737
QY 1441 CTAGTCTTTTCACTGCTGTGCAAGATTTAGGACACAATGTGGAGGTTATTTCTTCCAAAGT 1500
Db 2738 CAAGCTTTTCACTGCTGTGCAAGATTTAGGACACAATGTGGAGGTTATTTCTTCCAAAGT 2797
QY 1501 ACGGTGCTGATCTAGCAATGTCAGAAATCTACAAATCCATCAGAGTTTCTTGG 1560
Db 2798 ATGATTTGTTAATCTAAGCAGTGTGAAGGATTTTACACTACCAACAAAGTTTGTCTCGG 2857
QY 1561 GTGGTCTGMAATAATGTTGGCGTGGACTAGTCGAAGGCTTTGTGTTTACTTCTCTGG 1620
Db 2858 GTGGCAGAGATAAAGTATGTTTGGAAAGTTGAAGATCTGCAGTTTACTTCTTGG 2917
QY 1621 AACCTCAAAATGGGATGTTTGGAGTCCGATATGATATGGCAGGACGATACCCCGAT 1680
Db 2918 AACCAAAATGGCATGTTTGGGTTGGATGTTGATGGGAAGAATGATGAGAGTAGAT 2977
QY 1681 TTGGCTTCTCTGCTGCTCTAGAGTTCTCTCCTCCAAAGTGAATCTTCTCCGAACA 1740
Db 2978 TTGGCTTCTCTGCTGCTCTAGAGTTCTCTCCTCCAAAGTGAATCTTCTCCGAACA 3037
QY 1741 TAATACATTTGCCATGATGTTGTCAGTCTGTTGCTGGCTTACACAGGAAGAACTACG 1800
Db 3038 TCATACATTTGTCATGACTGTTCAAGTCTCCCGTCTGGCTTGGCTATACAGGAACGATG 3097
QY 1801 CGAAGTCTAGCTTGGCAACGACGCGGTGGTATTCACATCCACATCTTGAATTTGGAG 1860
Db 3098 CTCCTAATGGCTGGGAATGTTGGGTTGATGTTTACCATCCACATCTTGAATTTGGAG 3157
QY 1861 CGCATCATATTTGGCAAGCAATGAGATATTTGATATGAAGCAACACTGCTCTAATACAT 1920
Db 3158 CGCATCATATTTGGCAAGCAATGGCAATTTGTGACAAAGGCTCAACTGCTCTGATACAT 3217

QY 1921 ATTCAAAGGAAGTGTCCAGTTCATGTCCTCATAGTTCCTCATCTTGGAAATTCATGGCA 1980
Db 3218 ATTCAAAGGAAGTGTCCAGTTCATGTCCTCATAGTTCCTCATCTTGGAAATTCATGGCA 3277
QY 1981 TTCTCAATGAATGATTCGGATATATGGATCCGTCGATCAATGACAACTTTATCCCGTCC 2040
Db 3278 TTCCAAATGAATGATTCCTGACATTTGGGATCCATATACTGACAGATTTATTCGCGTTC 3337
QY 2041 ACTACATCTGTGAGATGTGTTGAAGGCAAGGCTGTAAAGAGGCGACTGCAGCAGA 2100
Db 3338 ATTATACATCAGAGAAATGTTCTTGAAGGCAAGGCTGTCAAAAAGGCAATTCGACAGA 3397
QY 2101 AGTTTGGGTTTACAGCAAAATCGATGTCCCGTCTGAGGAATCGTCACTTCGCTGACAGCC 2160
Db 3398 TGCTTGGATTTACAGCAAAATCGATGTCCCGTCTGAGGAATCATCACTTCGCTTAACAGTGC 3457
QY 2161 AAAAGGGGATCCACCTGATCAAGATGCGGATTCACCGTACACTCGAAGGCAAGCAGG 2220
Db 3458 AGAAGGGAATCCACCTTATCAAAATGCAATGATCGAGCTCTTGAACGCAATGGGCGAG 3517
QY 2221 TGGTTTTGCTTGTTCAGCGCGGACTCTCGAATCCAAAGCTGATTTTGTCAACCTGGCGA 2280
Db 3518 TGGTTTTTACTGGGTTCTGCACAGATCATCGCATCAAGGTGACTTTTACAAATTTAGCCA 3577
QY 2281 ATACGCTCCACGGCGTAAACCATGGGCAAGTGAAGGCTTTCTTGAACCTACGACGAGCTC 2340
Db 3578 GTAAGCTGCATGTTGATATACCATGGCGGGTGAAGCTATGTTTAACTATGACGAGCCAC 3637
QY 2341 TCTCGCATCTGATATACGCTGGCTCTGACTTCATCTGTTGGTCCCATCTATATTTGAGCCTT 2400
Db 3638 TGTCACATTT----- 3647
QY 2401 GCGGCTTAACTCAGCTCGTCCCATGGGTATGGAACCATCCCGATTTGTCGCAAGACTG 2460
Db 3648 -----GCTTATTGCTATGCGCTACGGATCCATCCCGATTTGTCGCAAGACTG 3694
QY 2461 GAGGCTCTTTCGACACTGTCTCGATGTGGAACAATGACAAGGAACGAGCGCGAGATCGAG 2520
Db 3695 GAGGCTCTTTCGACACTGTCTCGATGTGGAACAATGACAAGGAACGAGCGCGAGATCGAG 3754
QY 2521 GCCTTGAGCCCAACGGGTTTACGTTTACGAGGAGTGTAGCAACGCGTGTTCAGTACCGC 2580
Db 3755 GCCTTGAGCCCAACGGGTTTACGTTTACGAGGAGTGTAGCAACGCGTGTTCAGTACCGC 3814
QY 2581 TGAACAGGGCGATCTCAG 2598
Db 3815 TCGACAGAGCTATAACCG 3832

RESULT 12
VUA225088 3901 bp mRNA linear PLN 01-APR-1999
LOCUS Vigna unguiculata starch synthase isoform SS III.

DEFINITION
AJ225088
ACCESSION
AJ225088.1 GI:4582788
VERSION
KEYWORDS
SOURCE
ORGANISM
Vigna unguiculata (cowpea)
Vigna unguiculata

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Vigna.

REFERENCE
1
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
Bhullar, S.S., Willmitzer, L. and Kossmann, J.
Molecular cloning and characterization of major soluble starch
synthase (SS II) from cowpea (Vigna unguiculata)
Unpublished
2 (bases 1 to 3901)
Bhullar, S.S.
Direct Submission
Submitted (20-MAR-1998) Bhullar S.S., Molecular Plant Physiology,
Max-Planck Institut fuer Molekulare Pflanzenphysiologie,
Karl-Liebknecht Str. 25, Haus 20, 14476 Golm, GERMANY

FEATURES
source

Location/Qualifiers

1..3901
/organism="Vigna unguiculata"
/mol_type="mRNA"
/cultivar="C-88"
/db_xref="taxon:3917"
161..3604
/EC_number="2.4.1.21"
/function="ADP-glucose-starch glucosyltransferase"
/codon_start=1
/product="Starch synthase isoform SS III"
/protein_id="CAB40374.1"
/db_xref="GI:4582789"
/db_xref="GO:Q9XGC0"
/db_xref="SPTREMBL:Q9XGC0"
/translation="MEMSILQNYKTPFKFLKLPFSLTPSSWHKASIRVSCVNASADF
SRKQKQKSIAPKSPKSNPKVFKPSIGSSKKNPVKSGKSDSLAPVSEVLEDDNK
QTLVDIIDDDEPFSVEGVDKINKIAREBESSLIDETPDVENIPIIDVOLYE
EGNSVYDGDNGVSKSGBRLVYAEIDGNLGRVTDNGELAGNIVETSAAIDDDVIN
EASRMKLKLENLKQBIERIAENFLRGAKLFVYPPVXPDEIDIEFLKNLSTL
SDEPDLIIIGAFNDWENKGTIRLNKHLKDDWMSCOLYVPREAYKIDIEVFNQSVY
DNDQDFCIPVVGMDALVFDEFLKEKLEKLEKLAQERAEQRIIDADKA
VGEDELRQMEVEKMDTLQLQKNAVTSIDNVWYIEPSEFNDSVRLYNGNSGP
LOHAKVYVGNRGNKQDGLTI VERLVKSLGKGAWYADVVDQALVLDWVFAFGP
PQNAVYDNNRMDPEHIVPMATPDQYVVEBQLIVRKLQERKLEKEVIRAKBKT
AQKATKSKTLKFLLSQKHIVYTEPLDIQAGSTVYVYNSNTNLNRPVFRGS
FNWHRNGELPQRMPLPESGTHVRSVKVPLDIAITMDQFVSESENGGVFNDKQMD
YHLPVGGVIVKEPEMHI VHLAVEMAPIKVGGLGVVTSLSRAVDLNNHNDVILPKY
DCNLNSVDKLOPHKSPVGEI KYWHGKGLSVYFLEPQNGLEPVGCVYGRADA
ERPFCHALAEVLDLQNGHPDI ICHDWSAPVAVLFEKQYTHGLSKARVVFTTHN
LRFGANLIGKAMAYADKATPSYREIAGNHAVATHLKHGHIINGIDPIDWDFPN
DNSIPYVPAENVVEKRSKEALQKGLKADLPVGVITLTHQKHILHKLHAIW
RILBERGVLLGSAPDHRIQNDPVLNQLHSHNDRLCLAYDEPLSHMIYAGAD
FILVPSIFBFCQDITMRYGIPVIRKGTGLYTDVDDNDKDRQVQGLEPNFSG
FDGADAGGVYALNRAISAWYDGREWENTLCKTMEQDWSNRPALDYLELHYAACKL
E"

CDS

QY 482 AGCCAAAGGTTGAGGTAGACGACGAAGAAATAAATGTGCAATGTATTGGGTTTACCCAG 541
Db 1360 GGCAGAGATGAGAGGTTGAAAAAATGCAAGATACGTTGTGTCAGTTGATGAAAAATCCTGT 1419
QY 542 AGCTCCTGTTGATAATTTATGTGTACATTCAGGCCCATCAGCATGCGACAAAGAGGCTACTGT 601
Db 1420 AACCTCTATTGATAATGTTTGGTATATTGAGCCTAGTAGTTTAAACAGCAATGACTCAGT 1479
QY 602 CAGATTGTATTATAACATAAACTCAAGACCTCTAGTTTCAAGTACTGAGATATGATGCA 661
Db 1480 CAGATTATATTATAATGGAATCTGGGTCTCTTCAACATGCTTAAGGAAGTATGGGTCA 1539
QY 662 TGGTGGCTATAACAATTTGATGTGAGTCTCTTTTGTCTGTAAGGCTTGTTCATCA 721
Db 1540 TGGCGGTCAACAATTTGGAAGGATGGAATAAATGTGTGAAGGCTTGTCAAAACAGG 1599
QY 722 TGACAAAGATTGTGATTGGTGGTTTGCAGATGTGTCTGTCCTTGAAGAACATATGTATT 781
Db 1600 TTTGAAGAGTGGTCTTGGTGGTATGCTGATGTTGTGTACCTGACCAAGCTCTTGTCT 1659
QY 782 GGAATGGGTTTGTGTCAGCGGCCACACAGGAGTGCAGGAATATGACAAATGAGG 841
Db 1660 GGAATGGGCTTGTGCTGATGGTCCACTCAAAATGCAATGTGTATGATCAACAAACCGTAT 1719
QY 842 ACATGATTTTCATGCTACCTTCCAAATTAACATGACTGAGGAAGATATTGGATGGAAGA 901
Db 1720 GCAAGATTTCATGCTATTTGTCCTATGGCTACACCCGAGCGACAGTATTGGGTGAGGA 1779
QY 902 AGAACAAAGGATCTATACAGGCTTCAACAAAGAGAGAGGAGGAGGAGGAGGCTATTAA 961
Db 1780 AGAGCAGCTAATATACAGAAACTTCAGGAGGAGAGAGGTTGAAAGAGGATATACG 1839
QY 962 AAGGAAGGCTGAGAGAAATGCAAAAATGAAAGCTGAGATGAAGGAAAGAGCTATGAGAA 1021
Db 1840 GGCAGAGGCTGAAAAAACACAGCAAAATGAAAGCGGAAACAAAGGAGGAAACCTTTGAAAA 1899
QY 1022 GTTCTCTGTTTCTCAGAAACACATTTTACACGGAACCACTTGAATATACATCTGGAAC 1081
Db 1900 GTTTTCTATCTCAAAAGCATATCGTCTACACTGAGCCGCTGATATTCAAGCAGGAG 1959
QY 1082 TACTATTGATGCTTATAATCCTTCTAATACAGTTCTAACTGGAAGGCGCAGAGGTTTG 1141
Db 1960 TACAGTACGCTCTTTTATAAACCCCTCAACACAAATCTGAATGGAAGACCTGAGGTTG 2019
QY 1142 GTTTGATGTTCTTTAAATCGTTGGATGATTCAGGTGGGGTGTGCCACTCAGAGAT 1201
Db 2020 GTTTAGAGGCTCAATTAATCGTTGGTCTCATCGTAATGGTCCATGGCCACTCAGAGAT 2079
QY 1202 GGTACAGCAGAAATGGTTTCAACCTTAAAGCAACAGTTTACGTTCCACGAGATGCTA 1261
Db 2080 GTTGCCTGCTGAGAGTGGCACATGTCAAGGCTCTGTTAAAGTTCCATTTGATGATG 2139
QY 1262 TATGATGAGCTTCTGTTTCTCGGAGTCAAGAAAGGTGGAATTTATGATAACAGAAATGG 1321
Db 2140 CATGATGAGCTTTGTATCTCTGAGAGTGAATAATGGTGGAGTTTGTATAACAAATTTGG 2199
QY 1322 GTTAGACTATCATATTCCTGTTTTTGGGTCAATGTCAAGAGAACCACTTATGACATTGT 1381
Db 2200 AATGGATTACCATACCTGTTTTTGGAGTATTTGTGAAGGAAACCTCTATGATATTTGT 2259
QY 1382 CCACATTGCTGTTGAGATGGCACAATCGCAAGGTGGAGGTCTTGGTGTATGTTGTAC 1441
Db 2260 TCATATTGCTGTTGAGATGGCCCCAATTCGAAGGTTGGAGGCTTGGTGTATGTTGTAC 2319
QY 1442 TAGTCTTTTACGTCCTGTGCAAGATTTAGACCAATGTGGAGGTTTATTTCTCCAAAGTA 1501
Db 2320 TAGTCTTTCCGAGCTGTTCAAGATTTTAATCATTAATGTGGATATCATTTCTCCAAATA 2379
QY 1502 CGGTGCTTGAATCTAAGCAATGTCAAGATCTCAAAATCCATCCATCAGATTTTCTGGGG 1561
Db 2380 TGACTGCTTGAACCTTAGCAATGTAAAGGACTTGTGCAATTTTCAAAAAGCTATTCTGGAG 2439

ORIGIN

Query Match 46.9%; Score 1217.6; DB 8; Length 3901;
Best Local Similarity 67.0%; Pred. No. 0;
Matches 1743; Conservative 0; Mismatches 854; Indels 3; Gaps 1;
QY 2 GCTTGTGAAAAAATTTATTCGCTGGGAAACAAGTCTTCTTACTATCCAGATGATTGAA 61
Db 880 GATTGGAGGAAAAATTTTACAGAGGGCAAGTGTGTTGATATCTCTCTGTTGTTAA 939
QY 62 AGCTGATTCACAAATGATCTCTATTTCAATCGTGATCTATCATGCTGTGGCCATGAGCC 121
Db 940 ACCTGATGAAGATATACAGGTGTTTCTTAAACAAGAACCTTTCGACACATAAGTGATGAAC 999
QY 122 TGATGACTTATCAAGAGCATTCAATGGTGAAGTGGAGATTTTTCAGTGAATAAT 181
Db 1000 TGATATTGATTTGGGGCGTTTATGATGAGTGGAGTGAATAATCTTTTACCATTAGATT 1059
QY 182 GCACAGAGCGAGCTGCAGGGGACTGCTGCTGCTGCAAACTATACATCTCTAAGCAGGC 241
Db 1060 GAATAAACAACCTTAAAGATGATTTGGTGGAGTTGCCAATTTGATGTGCCAGAGAGC 1119
QY 242 ATACAGAAATGAGCTTGTGTTTTTAAACGACACACCGGTATATGAAATAATAACAATAA 301
Db 1120 CTATAAATAGACTTTGTGTTCTTAAATGACAAAGTGTATTGACAAATATGACCAAAA 1179
QY 302 TGATTTCTGATCAATAAGAACCACTGATGAAATTTTATTGAGGATTTCTTGGC 361
Db 1180 AGACTTTTGTATACCGATTTGTGTTGAATGGATGCAATTTGGTGTTCGAAGATTTTGTCT 1239
QY 362 TGAAGAAAGCAACGAGAACTTGAGAACCTTGCACAAATGAGGAAGCTCAAGAGGAGGACA 421
Db 1240 CGAGGAGAGCGTAAAGAAATTTAGAAAACCTTCTAAGGACGAGCTGAAGGGGAGACA 1299
QY 422 AACTGATGAGCAGCGCGCAATTTGAGGAGAAAGAGGCGCAGATTAAGCTGACGGGTACA 481
Db 1300 GGCTGAAAGAGCAAGGCGAATAGATGACACAAAGCTGTAAAGGAGGAGGACAGGTTGCA 1359

1231	TGATGCTTGGATATGGGAGCTTTTAAAGTAGTGGCGCTATAGTGTCTTTTACTACAAGGCT	1299
182	GCACAAGACGAGCTGGCAGGGACTGGTGGTGTGCAAACTATACATTCCTTAAGCAGGC	241
1291	AACGTAGACTCACTCAATGGAGATTGGTGGTCTTGCAGATCCATGTGCCAAGGAGC	1350
242	ATACAGAATGGACTTGTGTTTTTAAACGACACACGGTATATGAAATAATTAACAATAA	301
1351	ATACAGGGCTGATTTTGTGTTTTTAAATGACAAAGATGTCTATGACAACAATGATGGAA	1410
302	TGATTTGGTGATACAAATAGAAACACCATGGATGAAATTTATTTAGAGATTTCTTGGC	361
1411	TGACTTCAGTATACTGTGAAGGTGTGATGCAAAATCAITTGACTTTGAAATTTCTTGCT	1470
362	TGAAGAAAAGCAACGAGAACTTGAGAACCTTGCAAAATGAGAAAGCTGAAAGGAGGAGACA	421
1471	TGAGGAGAAATGGAGAGACAGGAGAACTTGCTTAAGAACAGCTGAAAGAGAAAGACT	1530
422	AACTGATGACAGCGCGGAATGGAGGAGAAAGGGCCGCGAGATAAAGCTGACAGGGTGACA	481
1531	AGCAGAAAGAACAAAGACGGAATAGAAAGCAGAGAAAGCTGAAATTCAGAGCTGACAGAGCACA	1590
482	AGCCAAAGTTGAGGTAGAGCAGAGAGAGATTAATTTGTGCAATGTAATTTGGTTAGCCAG	541
1591	AGCAAGGAGAGAGCTGCAAGAAAAAGAAAGTATTCGAGAAATGATGTGTAAGAGCCAC	1650
542	AGCTCTGTTGATTAATTTATGGTACATTTAGCCCCATCACGACTGGACAAGAGGCTACTGT	601
1651	GAAAGCTCGTGATACACCTGGTATACATAGAGCCAAAGTGAATTTAAATGCGAGGACAAGT	1710
602	CAGATTGTATTATAACATAAACTCAAGACCTCTAGTTTACAGTACTCAGATATGGATGCA	661
1711	CAGGTTATACTATAACAAAAAGTTTCAAGTCTCTCTCCATGCTAAGGACTTGTGGATCCA	1770
662	TGTTGGCTATACAAATTTGGATTGATGACTCTCTTTTGTGAAAGGCTTGTTCATCATCA	721
1771	CGGAGGATATAATTAATTTGGAGGATGGTTGTCTATTGTCAAAAGGCTTGTTAAATCTGA	1830
722	TGACAAAGATTGTCAATTTGGTGGTTTGCAGATGTTTGTCTGCTGAAAGAACATATGTATT	781
1831	GAGAAATAGATGGTGATTGGTGGTATACAGAGTTGTATTCTCTGATCAGGCACTTTCTT	1890
782	GGACTGGGTTTTTCTGACGGCCCCACAGGGAGTGCAAAGGAATTTATGACAACAATGGAGG	841
1891	GGATTGGGTTTTTCTGATGGTCCACCCAAAGCATGCCATTCCTTATGATAACAATCACCG	1950
842	ACATGATTTTCATGCTACCTTCCAATAACATGACTGAGGAGAGATTTGGATGGAGA	901
1951	CCAAAGACTTCCATGCCATTTGCCCAACCAATTTCCGAGAGAAATTAATTTGGTGTAGGA	2010
902	AGAACAAAGGATCTATACAAGGCTTCAACAGAGAGGAGGAGGAGGAGGAGGCTATATA	961
2011	AGAACATCAGATCTTTAGACACCTTCAGGAGGAGAGAGGCTTAGAGAGCGGCTATGCG	2070
962	AAGGAAGCTCAGAGAAATGCAAAAATGAAAGCTGAGATGAAGGAAAGACTATGAGAAT	1021
2071	TGCTAAGGTTGAAAAAACAGCACCTTCTGAAACCTGAAACAAAGGAAAGAACTATGAAATC	2130
1022	GTTCTGGTTTTCTCAGAAACACATTTGTTACACCGAACCACTTGAAATACATGCTGGAAC	1081
2131	ATTTTACTGTCTCAGAGAGCATGATATATACTGAACTCTTGATATCCAAGCTGGAAG	2190
1082	TACTATTGATGTCTTTATAATCTTTCTTAATACAGTTTCTTAACCTGAAAGCCAGAGGTTTG	1141
2191	CAGGCTCAGTTTTACTATAATCCGCCAATACAGTACTTAAATGGTAAACCTGAAATTTG	2250
1142	GTTTTCGATGTTCTCTTAAATCGTTGGATGATCCAGGTGGGGTGTGGCCACCTCAGAGAT	1201
2251	GTTCAGATGTTCAITTAATCGCTGGACTCACCGCTGGTCCATTGTCACCTCAGAAAT	2310
1202	GGTACAACAGAGAAATGTTTCAACCTTAAAGCAACAGTTTACGTTTCCACGAGATGCGTA	1261
2311	GTGCGCTGCTGAAATGGCACCATGTCCAGAGCAACTGTGAAGGTTCCATTTGGATGATA	2370

Qy	1262	TATGATGGAC	TTTCGTTTTCTCGGAGTC	AGAAAGAGT	GGMAATTTATGATACAGAAATCG	1322
Db	2371	TATGATGGAT	TTTTGTATTTTCCGAGAGAGAAGAT	TGTTGGGATTTTTTGACAAAT	TAAGAGCGG	2430
Qy	1322	GTTAGACTAT	CATATCTCTGTTTTTGGTCCAA	TGTGAAAGGAACCA	CCCTATGACAAATGT	1381
Db	2431	AATGGACTAT	CAATACCTGTGTTTGAGAGT	CGCTAAAGAACCTT	CCAATGCAATATGT	2490
Qy	1382	CCACATTTGCT	TGTGATGGCACCAAT	CGCAAAAGTTGGAGGT	CTTGGTGATCTTGTCA	1441
Db	2491	CCATATTTGCT	CGAAATGGACCAAT	TGCAAAAGTTGGAGGCT	TTGGTATCTTGTGTAC	2550
Qy	1442	TAGTCCTTT	CAGTCGTGTCAAGATTTAG	GACACAATGTGGAGGT	TATCTTCCCAAGTA	1501
Db	2551	TAGTCCTTT	CCGTCGTCTCAAGATTTAA	ACCATAATGTGGAT	TATCTTACCTAAGTA	2610
Qy	1502	CGGTTGCTT	GAATCTTAAGCAATCTCA	AGAAATCTCAAAATCCAT	CAGAGTTTTTCTTGGGG	1561
Db	2611	TGACTGTTT	GAAGATGAATAATGT	GAAGACTTTCGGTTTT	CACAAAACACTTTTTGGGG	2670
Qy	1562	TGGTTCTGA	ATAATTAATGTGTGGCGTG	CACTAGTCTGAAGGCTTT	TGTGTCTTACCTCCGGA	1621
Db	2671	TGGGACTG	AAATTAATTAATGTGGTT	TGGAAGGTGGAGGTCT	CTCGGTCTATTTTTTGGGA	2730
Qy	1622	ACCTCAAA	ATGGGATGTTTGGAGTC	GGATATGATATG---	GCAGGGAACGATCACCGCG	1678
Db	2731	GCCTCAAA	CGGGTATTTTCSAAAGGT	CGCTATGGTTGTAGCAAC	GAATGTTGAAACG	2790
Qy	1679	ATTTGGCTT	CTTCTGTCTGTCTAGAGTT	CTCCTCCAAAGTGGAT	CTCTCTCGAA	1738
Db	2791	ATTTGGTTT	CTTCTGTCA	CGGCTTTTGGAGTTTTCT	CTGCAAGGTGGATTTAGTCCGGA	2850
Qy	1739	CATTAATAC	ATTGCCATGATTTGGTCA	AGTGTCTCTGTTGCTCG	CTGCTCACAAAGAAACTA	1798
Db	2851	TATCAATTC	ATTGCCATGATTTGGTCT	AGTGTCTCTGTTGCTCT	TTTAAAGGAACAATA	2910
Qy	1799	CGCGAAGT	CTAGCTTGGCAAAACG	CAAGGTGGTATTCCACCAT	CCACAATCTTGAATTTGG	1858
Db	2911	TACACAT	TATGGTCTAAGCAAACT	CTCTATAGTCTTCA	CGATACATAATCTTGAATTTGG	2970
Qy	1859	AGCCATCAT	TATGGCAAAAGATGAT	TGTGATAAAGCAACACT	CTCTCTAATAC	1918
Db	2971	GGCAGAT	CTCATTTGGGAGCAATG	ACTAACGCAACAAGACT	CACAGCTTCCACCAAC	3030
Qy	1919	ATAATCAA	AGGAAGTGTCA	GTGTCATAGTTTCCCTCAT	CTTGGGAAATTTCTATGG	1978
Db	3031	TTACTCAC	AGGAGTGTCTGMAAAC	CCCTGTAAATTGCGCCT	CACCTTCAAGTTCCATGG	3090
Qy	1979	CAITTC	CAATGGAAATGAT	CGGANATATGGATCCGT	ACATGACAACTTTATCCCGT	2038
Db	3091	TATAGTGA	ATGGGATTCACCCAGAT	ATTTGGGATCTCTTAAAC	GAATGAATTCATTTCCGAT	3150
Qy	2039	CCACTAC	ACTTGTCTAGAAATGTGG	TTGAAGGCAAGAGGCTGCT	TAAAGGGCACTTGCAGCA	2098
Db	3151	TCCGTA	CACITTCAGAAAACG	TTGTTGAGGCAAAACAG	CGCCAGGAAGCTTTGCAAG	3210
Qy	2099	GAAGTTTGG	TTACAGAAATCGA	ATGTCCTCGGTAGGAAT	CGTCACTCGCTGACAGC	2158
Db	3211	AAAAC	TTTGGACTGAAC	CAGGCTGACCTTCTCTT	TGTAGGAATATCACCCGCTTAACTCA	3270
Qy	2159	CCAAAAG	GGGATCACTGTATCA	AGCATGGATTCACCGT	ACACTACCTGAAACGGACGACA	2218
Db	3271	CCGAAA	AGGAATCACCTCTATTA	ACATGCTATTTGGCG	CACCTTGGAAACGGAAACGGA	3330
Qy	2219	GGTGGTTT	TGCTTGGTTT	CAGCGCCGACCTCTCGA	ATCCAAAGCTGATTTTGTCAACCTTGGC	2278
Db	3331	GGTAGT	CTTGCTTGTTCTGCT	CTCTGATCTCTAGG	TACAAAACAAATTTTGTTAATTTGGC	3390
Qy	2279	GAATAC	CGCTCACCGGCTAA	ACCATNGGGCAAGT	GAGGCTTTCTTTGACTACGACGACC	2338
Db	3391	AAATCA	ATTTGACTTCCAAATAT	ATATGACCGCGACG	CACTGTCTGTCAACATATGACGACC	3450


```
QY 2339 TCTCTCGAHTGATATACGGTCTGACTTCTGCTTCTGCTCCCTATATTTGAGCC 2398
Db 3451 ACTTTCTCACCTGATATATGCTGCTGCTGATTTTATTTCTTCTCAATATTGAGCC 3510
QY 2399 TTGGGGCTTAAGTCTGCTGCGCATCGGTATGGAAACCATCCGATTGTCGCGCAAGAC 2458
Db 3511 ATGTGGACTACACAACTTACCGCTATGAGATGTTCAATCCAGTCGTGCGTAAAC 3570
QY 2459 TGGAGGGCTCTTCGACACTGCTTTCGATGTGGCAATGACAAAGAACGAGCCGAGATCG 2518
Db 3571 TGGAGGACTTTATGATGATCTGATTTGATGTTGACCATGACAAAGAGAGAGACCAACATG 3630
QY 2519 AGGCTTTCAGCCCAACGGTTTACGTTTACGGAGCTGATAGCAACGGTGTGACTAGC 2578
Db 3631 TGGTCTTGAACCAATGATTTCAGCTTTGATGGAGCAGATGCTGGCGGAGTTGATTATGC 3690
QY 2579 GCTGAACAGGGCGATCTCAG 2598
Db 3691 TCTGNATAGACTCTCTCTG 3710

RESULT 14
STSS 4127 bp mRNA linear PLN 27-AUG-1996
LOCUS S.tuberosum mRNA for starch synthase.
DEFINITION X95759.1 GI:1200153
ACCESSION X95759.1
VERSION starch synthase.
KEYWORDS Solanum tuberosum (potato)
SOURCE Solanum tuberosum
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1
AUTHORS Marshall,J., Sidebottom,C., Debet,M., Martin,C., Smith,A.M. and
Edwards,A.
TITLE Identification of the major starch synthase in the soluble fraction
of potato tubers
JOURNAL Plant Cell 8 (7), 1121-1135 (1996)
MEDLINE 96305754
PUBMED 8768372
REFERENCE 2 (bases 1 to 4127)
AUTHORS Edwards,A.
TITLE Direct Submission
JOURNAL Submitted (19-FEB-1996) A. Edwards, John Innes Centre, Colney Lane,
Norwich, Norfolk NR4 7UE, UK
FEATURES
source location/Qualifiers
1..4127
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Desiree"
/db_xref="taxon:4113"
/tissue_type="tuber"
/clone_lib="lambda gt11"
143..3835
/EC_number="2.4.1.11"
/codon_start=1
/product="glycogen (starch) synthase"
/protein_id="CAA65065.1"
/db_xref="GI:1200154"
/db_xref="GOA:Q43846"
/db_xref="SWISS-PROT:Q43846"
/translaton="MDVPRPLHRLSCTSVSNALTHLKIPILGFVSHGHTLSLVSQSS
SWRKGMTGVSEFICANSGRRRRKRVTPRSQSGSPKGFVPRKSGMSTQKVKQSN
GKSKSTSESEISNQTVEARVETSDDDTKGVVRDHFDEDEINGTKISM
SPVRSSQVSEETGGDDKDAVKLNKSESESGFIIDSVIREQSGQSTNASKG
SHAVGKLYEILQVDYEPQKLNNAVEYKPVASKLEITKASDVHTESNIDD
LQNSPFKGLDLEDEPLAAGVTGDSGLNLRLMEANLRRQAIERLAEENLLOQIR
LFCFPRVKPDEDEVEFLNRGLSTLNKESDVLIMGFANWRVRSFTTRLTETHLNGDW
WSCKIHVPKEARADRVFNGQDYDNDGNDFSIYKGMQIIDPENLLEKWRQ
EKLAEQAEERLAEESQRIEAEKIEADRAQAKKAKKKKRLRELKVKATKRD
TWYIEFSFKCEDKRLYLYNKSGPLSHADLWIHGGYNNKDGSLIVKLVKSERID
GOWWYEVVTPDQALELDVFDGPPKHAIAVDNNHRQDFHAIVPNHIPEELYWVEE
```

```
HOIFKTLQERRREAMRAKVEKTKALLTKETKERTMKSFLLSQKHVVYVTEPLDIQAG
SSVTVYNPANTVNLNGKPELWFRCSFNRTWTHRLGPELPQKMSPAENHVTVRATVKVPL
DAYMDFVPSEREDGGIFDNKSGMDYHLPVFGVAKPEPMHI VHIA VEMAPIAKVGL
GDVTVLSRAVDLNHNVDIILPKIDCLKNVKNDFPKHYFWGCTEIKWPEKVG
LSVYFLPEQNGLFSGKVCNSDGERFFCHAALEFLQGGFSPDIHCHDSSAP
VAMFLPEQYTHYGLSKSRIVFTIHNLEFAGDLI GRANTNADKATTVSTYSQVSGNP
VIAPLHFKFGHIVNGIDPDIWDLNDFGPIPIPTSENVVGKTAKEALQKGLQKA
DLPLVGTITLTHOKGHLIKHAIWRLERNGOVLLGSPADPRVQNVNFWNLANQLHS
KYNDARLCLTYDEPLSHLYAGADFLVPSIFEPCGLTOLTAMRYGSIIPVARTGGL
YDITVDVHDKERAQCGLEPNFSGDADAGDVYALNRALSALSWYDGRDWFNSLCKQ
VMSQDWSNWRPALDYDELYHAARKLE"
143..322
323..3832
sig_peptide
mat_peptide
/product="unnamed"
ORIGIN
Query Match 46.4%; Score 1206.4; DB 8; Length 4127;
Best Local Similarity 66.8%; Pred. No. 0;
Matches 1736; Conservative 0; Mismatches 861; Indels 3; Gaps 1;
QY 2 GCTTGCTCAAAAAAATTTATTCGCTGGGAAACAAGTTGTTTACTTATCCAGATGTATTGAA 61
Db 1111 GCTTGCCCGAGAAATTTATTGCAAGGATCAGATTTATTTGTTTCCAGAGTTGTAAA 1170
QY 62 AGCTGATTCAACAATGATCTCTATTTCATTCGTGATCTATCAGCTGTGGCCAAATGAGCC 121
Db 1171 ACTTGATGAAGATGTCGAGATATTTCTTAACAGAGGCTCTTCCACTTTTGAAGATGAGTC 1230
QY 122 TGATGTACTTATCAAGAGGACATTCATGGTGGAGTGGAGATTTTTCAGTGAATAATT 181
Db 1231 TGATGTCTTGATATGGGAGCTTTAATAGTGGCGCTATAGGCTCTTTTACTACAAGCT 1290
QY 182 GCACAAGAGCAGCTGGCAGGGGACTGGTGGTGTGCAAACTATATACATTCCTTAAGCAGGC 241
Db 1291 AACTGAGACTCATCTCAATGGAGATTGGTGGCTTGGCAAGATCCATGTTCOCAAGGAGC 1350
QY 242 ATACAGAAATGGACTTTGTGTTTTTAAACGACACACCGTATATGAAATATATAACAATAA 301
Db 1351 ATACAGGGCTGATTTGTGTTTTTAAATGGAACAAGATGCTATGACACAACATGATGAAA 1410
QY 302 TGATTTCTGTATACAAATAGAAAGCACCATGGATGAAATTTTATTTGAGGATTTCTTGGC 361
Db 1411 TGACTTCAGTATAAAGTGTGAAAGGTGGTGTGCAATCATTTGACTTTGAAAATTTCTTGT 1470
QY 362 TGAAGAAAAGCAAACGAGAACTTGAGAACTTGCAATACAGGAAGCTGAAAGAGAGAGACA 421
Db 1471 TGAGGAGAAATGGAGAGAACAGGAGAACTTGCTTAAAGAACAGCTGAAAGAGAGAACT 1530
QY 422 AACTGATCAGCAGCGCGGAATGGAGGAAAGAGGCGCCGAGATAAAGCTGCAGAGGTACA 481
Db 1531 AGCAGAAGAAACAAAGACGAATAGAGAGAGAAAGCTGAAATTTGAAGCTGCAGAGCACA 1590
QY 482 AGCCAAGGTTGAGGTAGAGACGAGAGAAATAAATTTGCAATGATTTGGGTTTACCCAG 541
Db 1591 AGCAAAAGGAGAGGCTGCAAGAGAAAGAGAGATTTGCGAGATTTGATGTTAAAGCCAC 1650
QY 542 AGCTCCTGTTGATAATTTATGTTACATTTGAGCCCATCAGCTGGCAAGAGGCTACTGT 601
Db 1651 GAAGACTCGTGATATCACCTGATACATAGAGCCAGTGAATTTAAATCGAGGACAAGT 1710
QY 602 CAGATTGTATTATATACATAAATCAAGACCTTAGTTACAGTACTGAGATATGATGCA 661
Db 1711 CAGGTTATATACATAAAGGTTTCAAGTCTCTCTCCATGCTAAGAGACTTGTGATGATCA 1770
QY 662 TGGTGGCTATACATTCAGTTGATGAGTCTCTCTTTGCTGAAAGGCTTGTTCATCATCA 721
Db 1771 CGGAGGATATAATAATTTGAGAGGATGGTTTGTCTATTGTCAAAAAGCTTGTTAATCTGA 1830
QY 722 TGACAAAAGATTTGATTTGGTGGTTTTGCAGATGTTTCTGCTGCTGAAAGAACATATGTA 781
Db 1831 GAGATAGATGTTGATTTGGTGGTATACAGAGGTTTGTATTCTCTGATCAGGCACCTTTCT 1890
QY 782 GGAAGTGGTTTTTGTGTGACGCGCCCAAGGAGTGAAGGAATTTATGACACAATGGAGG 841
```

1891 GATTGGGTTTGTGATGGTCCACCCAGCATGCCATTGCTTATGATAACAATCACCG 1950
1892 ACATGATTTTCAAGTACCTTTCCAAATAAATGATGAGGAAGATATGATGGAAGA 901
1951 CCAAGACTTCCATGCCATTTGTCACCAACACATTTCCGAGAGGAATATATTTGGGTTGAGGA 2010
902 AGAACAAAGGATCTATACAGGCTTCAACAAGAGGAGGGAAGGAGGAGGCTATTAA 961
2011 AGAACATCAGATCTTTAAGACACTTCAGAGAGGAGAGGCTTAGAGAGCGGCTATGCG 2070
962 AAGGAGGCTGAGAGAAATGCAAAATGAAGCTGAGATGAAGGAAAGACATATGAGAA 1021
2071 TGCTAAGGTTGAABAAACAGACTTCTGAABACTGAACAAAGGAAGAACTATGAATC 2130
1022 GTTCTCGGTTTCTCAGAAACATGTTTACACCGAACCACTTGAATACATGCTGGAAC 1081
2131 AATTTTACTGCTCAGAGCATGTAGTATATATCTGAACCTCTTGATATCCAAGCTGGAAG 2190
1082 TACTATTGATGCTTTATAATCCCTTCTAATACAGTTCTAATCGAAAGCCAGAGGTTTG 1141
2191 CAGGCTCAGATTTACTATAATCCCGCCAAATACGATCTTAATGTTAACTGAATTTG 2250
1142 GTTTCGATGTTCTTTAATCGTTTGGATGATCCAGGTGGGGTGTCCACCTCAGAAGAT 1201
2251 GTTCAGATGTTTCAATTAATCGCTGGACTCACCGCTGGGTCCATTGCCACCTCAGAAAT 2310
1202 GGTACAGCAGAAATGGTTTCAACCTTAAAGCAACAGTTTACGTTCCAGGAGATCCCTA 1261
2311 GTCCGCTGCTGAAATGGCACCATCTCAGAGCACTGTGAAGGTTCCATTTGGATGCATA 2370
1262 TATGATGAGTCTGTTTCTCGAGTCAAGAGGTTGGAATTTATGATAACAGAAATGG 1321
2371 TATGATGAGTCTGTTTATTTCCAGAGAGAGATGTTGGATTTTGAACAATGAGCGG 2430
1322 GTTAGACTATCATATTTCTGTTTGGGTCAATTTGCAAGGAACCACTTATGACATTTG 1381
2431 AATGGACTATCATATCTGTTTGGAGGAGTGGCTAAGAACCTTCCATGATATTTG 2490
1382 CCACATGCTGTTGAGATGSCACCAATCGAAGGTTGAGGTTTGGGTTGATGTTGTCAC 1441
2491 CCATATGCTGTCGAAATGGCAACCAATTCGAAGGTTGGGAGGCTTGGTATGTTGTAC 2550
1442 TAGCTTTTACGTCGCTGTGCAAGATTTAGGACCAATGTGAGGTTATTTCTTCCAAAGTA 1501
2551 TAGCTTTTCCGTCGCTTTCAAGATTTAACCATAATATGTTGATATATCTTACCTAAGTA 2610
1502 CGTTGCTTGAATCTAAGCAATGTCAAGATCTCAAAATCCATCAGAGTTTCTTGGGG 1561
2611 TGACTGTTTGAAGATGAATAATGTGAAGGACTTTCCGGTTTCACAAAACTTACTTTTGGGG 2670
1562 TGTTCTGAATAATGTTGTTGGGCTGACTAGTCGAGGCTTTGTTTACTTCTCTGGA 1621
2671 TGGGACTGAATAAATAGTATGTTTGGAAAGGTGGAAGGCTCTCGGCTCTATTTTGGGA 2730
1622 ACCTCAAAATGGGATGTTTGGAGTCGATATGATATG---GAGGAGCAGATCACGCCCG 1678
2731 GCCTCAAAACGGGTATTTTCGAAGGTTGGCTATGTTTGAACACGATGGTGAACG 2790
1679 ATTGGCTTCTTCTGCTGCTTCTGCTTAGAGTTTCTCCTCCAAAGTGGATCTTCTCCGAA 1738
2791 ATTGGTTTCTTCTGCTCAGCGGGTTTGGAGTTTCTTCTGCAAGGTGAATTTAGTCCGGA 2850
1739 CATATACATGCTGATGTTGCAACCGCAGGCTGGTATTCACCATCCACATCTTGATTTGG 1858
2851 TATCATTCATGTCATGATTTGTTAGTCTGCTGCTGTTGCTTCTTTAAGGAACAATA 2910
1799 CGGAGTCTAGCTTGGCAACCGCAGGCTGGTATTCACCATCCACATCTTGATTTGG 1858
2911 TACACATGTTGCTTAGCAAAATCTCGTATAGTCTTACGATACATATCTTGATTTGG 2970
1859 AGGSCATCATATTGGCAAGCAATGAGATTTGTGATAAGCAACAATGCTCTCTAATAC 1918

2971 GGAGATCTCATTTGGGAGAGCAATGACTAAACGACAGAAAGCTACACAGTTTCCACAA 3030
1919 ATATTCAAGGAAGTGTGAGTGTGATGTCATGTCCTATCTTTGGGAAATTTCTATGG 1978
3031 TTACTCAGAGGAGTGTCTGGAAACCCCTGTAATTTGGGCTTACCTTCAAGATTCCATGG 3090
1979 CATTTCAATGAAATTTGATCCGGATATATGGGATCCGTACAAATGACAACTTTATCCCGT 2038
3091 TATAGTGAATGGATTGACCCAGATATTTGGGATCCTTTAAACGATAAGTTTCAATCCGAT 3150
2039 CCACTACACTTGTGAAATGTTGTTGAAGGCAAGGGCTGCTAAGAGGCTACTGCAGCA 2098
3151 TCCGTACACTTTCAGAAAACGTTTGAAGGGCAAAACAGCAGCAAGAAAGCTTTTGACGG 3210
2099 GAAGTTTGGTTTACAGCAAAATCGATGTCCCGCTCGTAGGAATCGTTCACCTCGCTGACAG 2158
3211 AAACTTGGACTGAACAGGCTGACCTTCTTTTGGTGAATATACCCGCTTAATCTCA 3270
2159 CCAAAAGGGGATCCACCTGATCAAGCATCGGATCACCGTACACTCGAAGCGAAACGCA 2218
3271 CCAGAAAGGAATCCACCTCATTTAAACATGCTATTTGGCGCACCTTTGGAACGGAACGACA 3330
2219 GGTGTTTGTGTTGTTTGTGAGCCCGGACTCTCGAATCCAAAGCTGATTTTGTCAACCTGGC 2278
3331 GGTAGTCTTGTGTTGTTTGTGCTCTGATCCTAGGGTACAAAACAAATTTTGTAAATTTGGC 3390
2279 GAATAGCTTCCACGGCGTAAACCATGGGCAAGTAGGCTTTCCTTGACCTACGACGAGCC 2338
3391 AAATCAATTTGCACTCCAAATATATGACCGCGCACGACTCTGTCTAATATATGACGAGCC 3450
2339 TCTCTCGCATCTGATATACGCTGGCTCTCACTTCAATTTGGTCCCATCTATATTTGAGCC 2398
3451 ACTTTCTACCTGATATATGCTGGTCTGATTTTATTTAGTTCTTCAATATTTGAGCC 3510
2399 TTGCGGCTTAACTCAGCTCGTCGCCATGCGGTATGGAACCAATCCGATTTGTCGCAAGAC 2458
3511 ATGTGAGCTTAAACACAACTTACCGCTATGAGATGATGTTTCAATTTCCAGTCTGCTGTAAC 3570
2459 TGAGGAGCTTCTTCGACACATGCTTTCGATGTGACAAATGACAAAGAACGAGCCGAGATCG 2518
3571 TGAGGAGCTTATGATATGATCTGATTTGATGTTGACCATGACAAAGAGAGACACACAGTG 3630
2519 AGGCTTTGAGCCCAACGGGTTTGTAGCTTTGACGGAGCTGATAGCAACGGTGTGACTACGC 2578
3631 TGCTCTTGAACCAATATGATTTGAGCTTTGATGAGCAGATGCTGGCGGAGTTGATTTATGC 3690
2579 GCTGAACAGGGGATCTCAG 2598
3691 TCTGAATAGAGCTCTCTCTG 3710

RESULT 15

STSSIII
LOCUS S.tuberosum mRNA for soluble-starch-synthase.
DEFINITION
ACCESSION X94400
VERSION X94400.1 GI:19111165
KEYWORDS soluble starch synthase; SSSI gene.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum

REFERENCE 1
AUTHORS Abel,G.J., Springer,F., Willmitzer,J. and Kossmann,J.
TITLE Cloning and functional analysis of a cDNA encoding a novel 139 kDa starch synthase from potato (Solanum tuberosum L.)
JOURNAL Plant J. 10 (6), 981-991 (1996)
MEDLINE 97164391
PUBMED 9011082

2 (bases 1 to 4167)
REFERENCE
AUTHORS Abel,G.J.W.
TITLE Direct Submission

1535	TGAGGAAATGGAGAGAACGAGAGAAACTTCTGCTAAAGAACAAAGCTGAAAGAGAAAGACT	1591
422	AACTGATGACGACGCGCGAATGGAGGAAGAAAGGGCCGACAGATAAAAGCTGACAGGGTACA	481
1595	AGCGGAAGAACAAAGACGAATAGNAGCAGAGAAAGCTGAAATTTGAAGCTGACAGAGCAC	1654
482	AGCCAGGTTGAGGTAGACGACGAGAGAGAAATAATTTGTGCAATGTATTGGTTTACCCAG	541
1655	AGCAAGGAAAGAGGCTGCAAGAGAAAGAAAGATTTGCGAGAAATGATGTATAAAGCCAC	1714
542	AGTCTCTGTTGATAATTTATGTGTACATTCGAGCCCATCAGACTGGGACAGAGGCTACTGT	601
1715	GAAGACTCTGATATCACGTTGGTACATAGAGCCAAAGTGAATTTAAATGCGAGGACAAGT	1774
602	CAGATTGTATATAACAATAAACTCAAGACCTCTAGTTTCA CAGTACTGAGATATGGATGCA	661
1775	CAGTTATATCTAAACAAAGTTTCAGTGCTCTCTCCCATGCTTAAGGACCTGTGGATCCA	1834
662	TGTGTGCTATACAAAATGGATTGATCGACTCTCTTTTGTGAAAGGCTTCTTCATCATCA	721
1835	CGAGAGATATAAATTTGGNAGATGGTTTGTCTATTGTCAAAAGCTTGTTAAATCTGA	1894
722	TGACAAAGATTGTGATTTGGTGGTTTGCAGATGTTGTGCTCGCTGAAAGACAATATGATT	781
1895	GAGATAGATGGTGTGATTTGGTGGTATACAGAGGTGTGTAATTCCTGATCAGGCACTTCTT	1954
782	GGACTCGGTTTTGCTGACGGCCCCACCGAGGACTGCAAGGAATTTATGACAACTATGGAGG	841
1955	GGATTCGGTTTTTGTGATGGTCCACCAAGCATGCCATTCGTTTATGATAACAACTACCG	2014
842	ACATGATTTTCATGCTACCCCTTCCAAATACATGACTGTGAGAAAGATTTTGGATGGAAGA	901
2015	CCAAGACTTCCATGCCATTGTCCCCAAACACATTCGGAGAGAAATATATTGGGTTGAGGA	2074
902	AGAACAAAGATCTATCAGAGCTTCAACGAGAGAGGAGAAAGGAGAGGCTATTAA	961
2075	AGAACATCAGATCTTTAAGACACTTCAGGAGGAGAGAGGCTTAGAAGCGCGTATGCG	2134
962	AAGCAAGGCTGAGAGAAATCCAAAATGAAAGCTGAGATGAAGGAAAGACTATGAGAAAT	1021
2135	TGCTAGGTTGAAAACACGACCTCTGTAATACTGAAACAAAGGAAAGAACTATGAATC	2194
1022	GTTCCTGGTTTCTCAGAAACACATGTTGTTTACACGAAACCACTTGTAATAATGCTGGAAC	1081
2195	ATTTTTACTCTCTCAGAAGCATGTAGTATATATCTGAGCCTCTTGATATCCAAGCTGGAAG	2254
1082	TACTATTGATGTGCTTTATAATCTCTTAATACAGTTTCTAACTGGAAGCCAGAGGTTTG	1141
2255	CAGGTCACAGTTTACTATTAATCCGGCCAATACNGTACTTTAATGGTAAAACCTGAAATTTG	2314
1142	GT TTCGATGTTCTTAAATCGTTTGGATGTATCCAGGTGGGGTGTGCCACTCAGAAAGAT	1201
2315	GTTCAGATGTTCAATTAATCGCTGGACTCACCGCTGGGTCATTTGCCACTCAGAAAAAT	2374
1202	GGTACAGCAGAAAATGGTTTCACTTAAAGCAACAGTTTACTGTTCCACGAGATGCTTA	1261
2375	GTCCCTGCTGAAAATGGCAACCATGTGAGAGCAACTGTGAAGTTTCCATTGGATGCAATA	2434
1262	TATGATGGAATTCGTTTTTCTCGGAGTCAGAAAGAGGTGGAATTTATGATAACAGAAAATGG	1321
2435	TATGATGGAATTTTGTATTTTCCGAGAGAGAAGATGGTGGGATTTTTCACAATAAGAGCGG	2494
1322	GTTAGACTATCATTTCTCTGTTTTTGGGTCAATTCGAAAGGAACCACTATGCACATTGT	1381
2495	AATGGACTATCACATACCTGTGTTTGGAGAGTCGCTTAAAGAAACCTCCAATGCATATTGT	2554
1382	CCACATTTGCTTTGAGATGACCAACATCGCAAGTTTGGAGGTCCTTGCTGATGTTGTAC	1441
2555	CCATTTGCTGTGAAATGACCAAAITGCAAGGTGGGAGGCTTGCTGATGTTGTATC	2614
1442	TAGTCTTTACGTGCTGTGCAAGATTAGACACAAATGTCGAGGTATTCTTCCAAAAGTA	1501
2615	TAGTCTTTCCGTTGCTTTCAAGATTTAAACCAATAATGTGGATATTCTTACCCTAAGTA	2674

QY 1502 CGGTTCCTTGAATCTAAGCAATGTCAAGAAATCTAAGAAATCCATCAGAGTTTCTTGGGG 1561
Db 2675 TGACTGTTTGAAGATGAATAATGTGAAGGACTTTCGGTTTCAAAAAACTCTTTTGGGG 2734
QY 1562 TGGTTCTGAAATAAATGTGTGGCGTGCAGTGTAGTGAAGGCCCTTTGTGTTTACTTCTCTGA 1621
Db 2735 TGGGACTGAAATAAAGTATGTTTGAAGGTGAAGTCTCTCGTCTATTTTGTGA 2794
QY 1622 ACCTCAAAATGGGATGTTTGGAGTCGGATATGATATG--GCAGGAGCATGACCGCG 1678
Db 2795 GCCTCAAAACGGGTTATTTTCGAAAGGGTGGCTATGTTGTAGCAATGATGGTGAACG 2854
QY 1679 ATTGGCTTCTTCTGTCGTCTCTGCTAGAGTTTCTCTCCAAAGTGGATCTTCTCGAA 1738
Db 2855 ATTGGTCTTCTCTGTCACGCGGCTTTGGAGTTTCTCTGCAAGGTGGATTTAGTCCGA 2914
QY 1739 CATAATACATTTGCCATGATTGGTCAAGTGTCTCTGTTGCTGGCTACAAAGGAAACTA 1798
Db 2915 TATCATTTCAATGGCATGATTGGTCTAGTGTCTCTGTTGCTTAAAGGAACAATA 2974
QY 1799 CGGAAATCTAGCTTGGCAAAACGACGGGTGATTCACCAATCCAAATCTTGAATTTGG 1858
Db 2975 TACACACTATGGTCTAAGCAAACTCGTATAGTCTTCAAGATACATAAATCTTGAATTTGG 3034
QY 1859 AGGCATCATATTGGCAAGCAATGAGATATTGTGATAAGCAACAATCTCTCTAATAC 1918
Db 3035 GGCAGATCTCAATTTGGGAGAGCAATGACTAACCGAGACAAGCTACAACTTTCACCAAC 3094
QY 1919 ATATTCAAAAGGAAGTCTCAGGTGATGTCCTGTTGCTGGCTACAAAGGAAATCTATGG 1978
Db 3095 TTACTCACAGGAGTGTCTGGAACCCCTGTAATTTGGCTCTACCTTCAAGSTTCCATGG 3154
QY 1979 CAATCTCAATGGAATTTGATCCGGAATATAGGATCCGTACATGACAACTTTATCCCGGT 2038
Db 3155 TATAGTGAATGGGATTTGACCCAGATATTTGGGATCTCTTAAACGATAAGTTCAATCCGAT 3214
QY 2039 CCACCTACCTGTGAGAAATGTGTTGAAGCAAGAGGGTCTTAAGAGGCACTGCAGCA 2098
Db 3215 TCCGTACCTCTGAAACCGTGTGTAAGGCAAAACAGCAGCCAGGAAGCTTTGCAGCG 3274
QY 2099 GAAGTTTGGGTTACAGCAAAATCGATGTCCCGCTCGTAGGAATCGTCACTCGCCTGACGC 2158
Db 3275 AAAACTTGGACTGAACAGSCTGACCTTCTCTTTGGTAGGAATTTACCGCGCTTAACCTCA 3334
QY 2159 CAAAAGGGGATCCACTGATCAAGCATGCGATTCACCGTACACTCGAACGGAACGAC 2218
Db 3335 CCAGAAAGGAATCCACTCAATTAACATGCTATTTGGCGCACCTTGGACGGAACGAC 3394
QY 2219 GGTGGTTTGTCTTGGTTTTCAGCGCGGACTCTCGAATCCAAAGCTGATTTTGTCAACCTGGC 2278
Db 3395 GGTAGTCTTGTCTTGGTTTCTGCTCTGATCTCTAGGTACAAAAGATTTTGTAAATTTGGC 3454
QY 2279 GAATACGCTCCACGGGTAAACCATGGGCAAGTAGGCTTTCTTGTGACCTTACGACGAGCC 2338
Db 3455 AAATCAATTGCACTCCAAATATAATGACCGCGCACGACTCTGTCTAACATATGACGAGCC 3514
QY 2339 TCTCTCGCATCTGATATACGCTGGCTCTGACTTCAATCTGGTCCCATCTATATTTGAGCC 2398
Db 3515 ACTTCTCAGCTGATATATGCTGGTGTGATTTTATTTCTAGTTCTCTCAATATTTGAGCC 3574
QY 2399 TTGGGCTTAACCTCAGCTCGCTCGCATGGGTATGGAACCATCCGATTTCTCGCAAGAC 2458
Db 3575 ATGTGACTTAACAACTTACCGCTATGAGATATGGTTCAATTTCCAGTCTGGGTAAAC 3634
QY 2459 TGGAGGGCTCTTCGACACTGCTCTTCTGATGTGGAATGACAAAGGAACGAGCCCGAGATCG 2518
Db 3635 TGGAGGACTTTATGATACTGTAATTTGATTTGACCTATGACAAAGAGAGAGACACACAGTG 3694
QY 2519 AGGCTTTGAGCCCAACGGGTTTACCTTTGACGAGCTGATAGCAACGGTGTGACTACGC 2578
Db 3695 TGGTCTTGAACCAAAATGGATTCAGCTTTGATGGAGCAGATGCTGGCGGAGTTGATTATGC 3754

QY 2579 GCTGAACAGGGCGATCTCAG 2598
Db 3755 TCTGAATAGAGCTCTCTCG 3774

Search completed: June 20, 2004, 10:07:31
Job time : 16055 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 20, 2004, 01:59:08 ; Search time 1450 Seconds

(without alignments)

7611.599 Million cell updates/sec

Title: US-10-634-262-1_COPY_2425_5022

Perfect score: 2598

Sequence: 1 agctgtcgtaaaattat.....gctgaacaggcgatctcag 2598

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseqn 29Jan04: *
1: geneseqn1980s: *
2: geneseqn1990s: *
3: geneseqn2000s: *
4: geneseqn2001as: *
5: geneseqn2001bs: *
6: geneseqn2002s: *
7: geneseqn2003as: *
8: geneseqn2003bs: *
9: geneseqn2003cs: *
10: geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2598	100.0	6027	2	AAX58751 Maize dul
2	2598	100.0	6027	7	ABX09935 DNA encod
3	1766.6	68.0	5346	3	AAC86413 Wheat sta
4	1744.2	67.1	3621	3	AAC86414 Wheat sta
5	1703.8	65.6	5760	7	ADAC69827 Rice gene
6	1646.8	63.4	3645	7	ADA70734 Rice gene
7	1581.4	60.9	3032	9	ADC07865 Rice DNA
8	1500.4	57.8	4121	5	Aaf61270 Maize sta
9	1204.8	46.4	4127	2	AAT68646 Potato so
10	1141.2	43.9	3078	7	ADA68321 Arabidops
11	931	35.8	2301	2	AAT32324 Soluble s
12	501	19.3	2446	3	AAC86416 Wheat sta
13	501	19.3	11611	3	AAC86432 Wheat SSI
14	290.6	11.2	548	6	AAD33325 Rice star
15	207.6	8.0	437	6	AAD33324 Rice star
16	197.6	7.6	1032	3	AAC86417 Wheat sta
17	183.8	7.1	297	6	ABL73972 Corn tass
18	176.4	6.8	299	6	ABL74146 Corn tass
19	175	6.7	212	7	ABX81641 Corn ear
20	145	5.6	2652	2	AAT75137 DNA encod
21	145	5.6	3430	9	AAD60671 Corn star
22	144.8	5.6	3434	6	ABS52829 Maranta a
23	140.8	5.4	1275	4	AAS00044 Wheat CDN

24	140.8	5.4	1275	9	AAD60675	Aad60675 Wheat sta
25	140.8	5.4	3386	9	AAD60676	Aad60676 Wheat sta
26	140.4	5.4	1592	3	AAC86420	Aac86420 Wheat sta
27	137.6	5.3	759	9	ADC08765	Adc08765 Wheat DNA
28	136.2	5.2	240	6	ABL73926	Ab173926 Corn tass
29	134.4	5.2	3453	9	AAD60673	Aad60673 Rice star
30	133	5.1	871	3	AAC86419	Aac86419 Wheat sta
31	125.2	4.8	2865	7	ADA70571	Ada70571 Rice gene
32	122.4	4.7	892	3	AAC86418	Aac86418 Wheat sta
33	112.4	4.3	165	9	ADC08820	Adc08820 Corn DNA
34	111.8	4.3	2380	2	AAV66834	Aav66834 Zea mays
35	110.8	4.3	2478	2	AAT67287	Aat67287 Soluble s
36	110.2	4.2	2622	7	ADA69445	Ada69445 Rice gene
37	106.8	4.1	579	9	ADC08619	Adc08619 Banana DN
38	92.2	3.5	2115	3	AAC32824	Aac32824 Arabidops
39	87	3.3	2179	7	ABQ80055	Abq80055 Soybean g
40	86.8	3.3	2423	2	AAV70958	Aav70958 DNA encod
41	85.6	3.3	2097	2	AAV29755	Aav29755 Zea mays
42	85.6	3.3	2480	7	ABX09934	Abx09934 DNA encod
43	79.6	3.1	1984	3	AAC46797	Aac46797 Arabidops
44	77.4	3.0	2202	6	ABS52823	Abs52823 Curcuma z
45	76	2.9	2946	6	ABK88115	Abk88115 cDNA enco

ALIGNMENTS

RESULT 1

AAX58751
ID AAX58751 standard; cDNA; 6027 BP.

XX AAX58751;

DT 16-AUG-1999 (first entry)

DE Maize dull1 gene encoding starch synthase enzyme DUL.

KW Starch synthase; SSII; DUL; dull1 gene; maize; transgenic plant; ss.

XX Zea mays.

XX Key Location/Qualifiers

FT misc_feature 1..1437

FT /tag= f

FT /note= "functional fragment of cDNA specifically claimed

FT in Claim 16"

FT CDS 120..5147

FT misc_feature

FT /tag= a

FT 120..1221

FT /note= "functional fragment of cDNA specifically claimed

FT in Claim 12"

FT /tag= .816

FT misc_feature

FT /tag= d

FT /note= "functional fragment of cDNA specifically claimed

FT in Claim 14"

FT /tag= .1221

FT misc_feature

FT /tag= c

FT /note= "functional fragment of cDNA specifically claimed

FT in Claim 13"

FT /tag= .1944

FT misc_feature

FT /tag= e

FT /note= "functional fragment of cDNA specifically claimed

FT in Claim 15"

FT /tag= g

FT /note= "functional fragment of cDNA specifically claimed

FT in Claim 17"

FT /tag= .3791

FT misc_feature

FT /tag= h

FT /note= "functional fragment of cDNA specifically claimed

FT in Claim 18"

composition, and to screen plants to identify mutations which affect starch content and composition. The starch can then be used in food products, such as flour, and in films, coatings, adhesives, building materials and packaging materials.

Sequence 3621 BP: 1060 A: 697 C: 904 G: 959 T: 0 U: 1 Other:

Query Match	67.1%	Score 1744.2	DB 3	Length 3621	
Best Local Similarity	80.2%	Pred. No. 0			
Matches 2085	Conservative	0	Mismatches 509	Indels 6	Gaps 3
QY	1	AGCTTGCTGAGAAAAATTATTTCGCTGGGAAACAAGTTGTTTACTTATCCAGATGTTATGA	60		
DB	455	AATCGCTGAGAAAAATTATTCGATGGGAACAAGCTGTTTGTCTTCCAGAGTAGTGA	514		
QY	61	AAGCTGATTCAACAATTGATCTCTATTTCATCTGATCTATCAGCTGTGGCCATGAGC	120		
DB	515	AAGCTGATTGAGTTATTTGATCTTTATTATAAATCGTGACCTAACAGCTTTTGGCGAATGAAC	574		
QY	121	CTGATGTCTTATCAAGAGGACATTCATCGGTGGAGTGGAGATTTTTCACATGAAAAAT	180		
DB	575	CCGATGTCGTATCAAGAGGACATTCATCGGTGGAAATGGAGCTTTTCACTGAAAGAT	634		
QY	181	TGCACAAAGACGAGCTGGCAGGGGACCTGCTGGTCTGCAAACTATACATTCCTAAAGCAGG	240		
DB	635	TGCACAGAGTGACCTTGGAGGGGTTTGGTGGCTTGCBAACCTGTCATACCCAGGAGG	694		
QY	241	CATACAGAAATGGACTTTGTGTTTTTAAACGGGACACACGGTATATGAAAAATATAACAATA	300		
DB	695	CCTACAGATTAGACTTTGTGTTCTTCAACGGTGGCAGCGTCTATGAGAACAAATGGCAACA	754		
QY	301	ATGATTTTCGTGATCAACAATAGAAGCACCATGGATGAATAATTTATTGTAGGATTTCTTGG	360		
DB	755	ATGATTTCTGTATAGGAATAGAGGCCTATGAATGAAGATCTGTTGTAGGATTTCTTGG	814		
QY	361	CTCAAGAAAAAGCAACGAGAACTTGAGAACCTTGCAAATGAGGAAGCTGAAAGAGGAGAC	420		
DB	815	TTAAAGAAAGCAAGGAGCTTGAGAAACTTGCCATGGHAGAAGCTGAAAGGAGGACAC	874		
QY	421	AAACTGATAGCAGCGCGAATGGAGGAAGAAAGGCGCGCAGATAAAGCTGACAGGGTAC	480		
DB	875	AGACTGAAGAACAGCGCGCGAAGAAAGAACGAGGGCTGCAGATGAAGCTGTTCAGGGCAC	934		
QY	481	AAGCCAAAGTTGAGTGAGACGAAAGAGAAATAAATTTGCAATGTAATGGGTTTAGCCA	540		
DB	935	AAGCGAAGCGGAGATAGAGATCAAGAAAGAAAATTTGCAAGTATGTTGAGTTTGCCA	994		
QY	541	GAGCTCCTGTGATAATTTATGGTPACATTCAGCCCATCAAGCTGGGACAGAGGCTACTG	600		
DB	995	GAACTGTGTTGATAATTTGTGGTPACATAGAGGCTAGCACAGATACAAGAGGAGATACTA	1054		
QY	601	TCGATTTGATTTATAACATAAACTCAGACCTCTAGTTTACAGTACTTGAGNATGGATGC	660		
DB	1055	TCAGGTTATATTATAACAGAAACTCGAGGGCCACTTGGCCATAGTACGTAGATTTGGATGC	1114		
QY	661	ATGGTGGCTATAACAATTTGATTCATCGACTCTCTTTTGTGTAAGGCTTGTTCATCATC	720		
DB	1115	ATGGTGGTTACACAATTTGTCAGATGGACTCTCTATTTGTTGAAGCTTTGTCAAGTGCA	1174		
QY	721	ATGACAAAGATTTGATTTGGTGGTTTTGCAGATGTTGTCGTGCCCTGAAAGAACATATGAT	780		
DB	1175	ATGACAAAGACGGCGATTGGTGGTATGCAGATGTTATTCACCTGAAAAGGCACTTGTGT	1234		
QY	781	TGGACTGGGTTTTGCTGACGGGCCACCGAGGATGCAAGGAATATGACACAAATGGAG	840		
DB	1235	TGGACTGGGTTTTTGTGATGGGCCAGCTGGGAATGCAAGGAAGCTATGACACAAATGCTC	1294		
QY	841	GACATGATTTTTCATGCTACCCCTTCCAAATAACA--TGACTGAGGAAGAGTATTGGATGG	897		
DB	1295	GACAAGATTTCCATGCTATTCTTTCCGAACAACAATATGTAACGAGGAGGCTTCTTGGGCGC	1354		
QY	898	AAGAAGAACAAAGGATCTATACAGGCTTCAACAGAGAGGAGGAGGAAAGGGAAGGAGCTA	957		

3368 ATGACGAAATGGTATGTTGGTATGCTAATGTTTCATATACCTGAAAGGCCCTTTGTAT 3427
781 TGGACTGGTTTTGCTGACGGCCACCAGGAGTGCAAGGAATATGCAACAATGGAG 840
3428 TGGACTGGTTTTGCTGACGGGCCACCTGGAATGCAAGGAATATGCAACAATGGTC 3487
841 GACATGATTTTCATGCTACCTTCCAAATAACATGACTGAGGAAGAGATTTGGATGGAG 900
3488 GACAAGATTTTCATGCTATTTCCAAATGCGATGACTTAACGAAGAATATTTGGGTGAAG 3547
901 AAGAACAAAGATCTATACAGGCTTCAACAGAGAGAGGGAAGGAGGAGGCTATTATTA 960
3548 AGGAAGCTGATCTATACAGGCTTCTCCAGAGATCAGAGAACGGAGGAGGCTATTATTA 3607
961 AAAGGAGGCTGAGAGAATGCAAAATGAAAGCTGAGATGAAGGAAGAAAGACTATGAGAA 1020
3608 AATTAAGGTTGAGAAAGAGCAAAATGAAATCTGAGATGAAGGAAGAAAGACTATGAGAA 3667
1021 TGTTCCTGGTTTCTCAGAAACACATTTGTTTACCGAACCTTGAATATACATGCTGAA 1080
3668 TGTTCCTACTTCTCAGAAACACATTTGTTTATCTGAAACCTTGAATATACATGCTGAA 3727
1081 CTACTATTGATGCTTTATATCTTCTTATACAGAGTTCTAATGCAAGTTTCACTGAAAGCCAGAGTTT 1140
3728 CAAGTGGATGTTCTATATATATCTTCTTATACCGGCTGCTGAATGGAAGCCAGAGTTT 3787
1141 GGTTCGATGTTTCTTATATCTGATGTATCCAGGTTGGGTTGTCACCTCAGAAGA 1200
3788 GGTTCGATGTTTCTTATACCGATGATGATCCAGTGTCTTACCAAGTGTCTTACCAAGCAAGA 3847
1201 TGGTCAAGCAGAAATGGTTTCACTTAAGCAACAGTTTACGTTCCACAGATGCTT 1260
3848 TGGTCAAAACAGAAATGGTTTCACTTAAAGCCAGACAGTTTACGTTCCATCGGATGCTT 3907
1261 ATATGATGATGCTTCTGAGTCAAGAGAGAGTGGAAATTTATGATAACAGAAATG 1320
3908 ATATGATGATGCTTCTGAGTCAAGAGAGAGTGGAAATTTATGATAACAGAAATG 3967
1321 GGTGATGATCATATCTCTGTTTTTGGTCAATTTGCAAGGAACCACTATGCAATTTG 1380
3968 GACAGACTATCATATCTCTGTTTTCTGTTTCCAATGCAAGGAGCCTCCCATTCATATTG 4027
1381 TCCATGCTGTTGATGAGTGGCAACCAATCGCAAGTTGAGGCTCTGTTGATGTTGCTCA 1440
4028 TCCATATACGGTTGAGATGGCAACCAATGCAAGTTGAGGCTCTGTTGATGTTGCTCA 4087
1441 CTAGTCTTTCACTGCTGTGCAAGATTTAGGACACAATTTGCAAGTTTATTTCTTCAAGT 1500
4088 CAAGTCTTTCACTGCAATTTCAAGAGTTAGGCCATCATGTTGAGTTTATTTCTCCGAAT 4147
1501 ACGGTTGCTTGAATCTAAGCAATGTCAGAAATCTCAAAATCCATCAGAGTTTCTTTGG 1560
4148 ATAAATTTTATGAATCAAGCAATGTCAGAAATTTGCAATGTCAGAAATTTCTTTTGG 4207
1561 GTGGTTCTGAATTAATGTTGGCTGAGTCTGAGGCTTCTGTTTACTTCTCTG 1620
4208 GTGGTACAGAAATTAAGTGTGTTTGGATGATGAGGAGCCTGCTGTTTACTTCTTGG 4267
1621 AACCTCAAAATGGGATGTTTGGAGTGGATATGATATGCGAGGACGATGACCGCGAT 1680
4268 AACCTCAAAATGGGATGTTTGGGTTGGATGATATGAGGGAACGATGCTGGCAGAT 4327
1681 TTGGCTTCTTCTGCTGTTGCTCTAGAGTTTCTCTCCAAAGTGGATCTTCTCCGACA 1740
4328 TTGGCTTCTTCTGCTGCTCTAGAGTTTCTCTCTTCCATGAGTGGATCTTCTCCACATA 4387
1741 TAATACATTCGCTGATGTTGCTGAGTCTCTGTTGCTGCTGCTACACAAGGAATCTACG 1800
4388 TAATACATTCGCTGATGTTGCTGAGTCTCTGTTGCTGCTGCTATACAAGGAACACTATG 4447
1801 CGAAGTCTAGCTTGGCAAAACGACGGGTGGTATTTACAGCTCCCAATCTTTGAATTTGGAG 1860
4448 CAGATCCAGGTTGGCAACTGCGCGGATATATTTACCATCCATAATCTTGAGTTGGAG 4507

QY 1861 CGCATCATATTTGGCAAGCAATGAGATATTTGTATTAAGCAACAACCTGCTCTTAATCAT 1920
Db 4508 CACATTTTATTTGAAAACCAATGACATCTGCGCAAAAGCCACAACTGTTTCTCACAGT 4567
QY 1921 ATTCAAAAGGAAGTGTCAAGTCAATGGTGCCATAGTTCCCTCATCTTTGGGAAATTTCTATGGCA 1980
Db 4568 ATTCAAAGGAAGTGTCAAGTCAATGGTGCCATAGTTCCCTCATCTGTTGGGAAATTTCTATGGAA 4627
QY 1981 TTCTCAATGGAATTTGATCCCGATATATGGGATCCGTACAATGACAACTTTATCCGGTCC 2040
Db 4628 TTCTCAATGGAATTTGATCCCGATATCTGGGATCCATATCTGATAAATCTTATCCCGATGC 4687
QY 2041 ACTACACTTTGAGAAATGTTGTTGAAGCAAGAGGCTGCTTAAGAGGCACTGACAGAGA 2100
Db 4688 ATTATATCTTCTGAAATTTGTTGAAGCAAGATGCTGCAAGAGAGCANTTGACAGAGA 4747
QY 2101 AGTTTGGGTTACAGCAATCGATGTCCTCCGTCGTAGGAATCGTCACCTCCCTGACAGCCC 2160
Db 4748 GTTTGGACTGACAGACTGATGTCCTCCATTTGTTGGAATCATCACTGCTGACAGCCC 4807
QY 2161 AAAAGGGGATCCACTGATCAAGCATGCGATACCGTACACTCGAACGGAACGACAGAG 2220
Db 4808 AGAAGGGTATCCACTTAAACATGCACTTCACTCGGACACTTTGAACGCAATGGACAGG 4867
QY 2221 TGGTTTTGTTGTTTCAGGCGCGGACTCTCGAATCCAAAGCTGATTTTGTCAACCTGGCGA 2280
Db 4868 TGGTTTTGTTGTTTCAGCTCCAGATCCTCGGATACAGAGTATTTCTGCAGATTGGCTG 4927
QY 2281 ATACGCTCCAGCGGCTAAACCATGGGCAAGTGAGGCTTTTCTTTGACCTACGACGAGCCTC 2340
Db 4928 ATAGTCTTCATGGTGAACCATG----- 4952
QY 2341 TCTCGCATCTGATATACGCTGCTCTGACTTCAATTTCTGTCCTCATCTATTTTGGACCTT 2400
Db 4953 -----CAGGATATGCTGGCTCTGACTTCACTTCTGTTCCATCCATCCATTTGAACCTT 5005
QY 2401 GGGGCTTAACCTCAGCTCGCTCGCCATGCGGATGGAACCATCCGATTTGTCGCAAGACTG 2460
Db 5006 GGGGTTGACTCAACTGTTTGCATGCGCTATGGATCCATCCCTATTTGTCGGAACCG 5065
QY 2461 GAGGCTCTTCCACACTGTTTTCGATGTGGACAATGACAAGGAACGAGCCGAGATCGAG 2520
Db 5066 GAGGCTTTACGACACTGTTTTCGACGTAGACCAATGACAAGACCGGCTCGAGTTCTAG 5125
QY 2521 GCTTTGAGCCCAACGGGTTTACCTTTGACGAGCTGATAGCAACGCTGTTGACTAGCGC 2580
Db 5126 GCTTTGAACCAATGGGTTTCAGCTTTGATGAGCTGACTGTAATGTTGTTGATTTACGCC 5185
QY 2581 TGAACAGGCGGAT 2593
Db 5186 TGAACAGGCAAT 5198

RESULT 6
ADA70734
ID ADA70734 standard; DNA; 3645 BP.
XX ADA70734;
XX AC
XX 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 4057.
XX Plant; bacterial infection; fungal infection; viral infection; rice;
XX gene; ds.
XX Oryza sativa.
XX OS
XX WO200300898-A1.
XX
XX PD
XX 03-JAN-2003.

QY	1681	TTGGGCTCTTCTGCTCGTCTCTAGAGTTTCTCCTCAAAGTGGATCTTCTCCGAACA	1740
DB	2606	TTGGGCTCTTCTGCGCAATCTGCTCTAGAGTTTCTCGGCAAAATGGATCTTCTCCTGATA	2665
QY	1741	TAATACATTTGCCATGATTTGGTCAAGTGTCTCTGTTTCCCTGGCTACACAAGGAAACATACG	1800
DB	2666	TTATACATTTGTCTATGATTTGGTCAAGTGTCTCAAGTTTGTCTGGCTATTCAAGGAAACAATATG	2725
QY	1801	CGAAGTCTAGTTGGCAACGCAACGGTGGTATTCCACATCCACAACTTTTGAATTTGGAG	1860
DB	2726	CTCAAAATGSACTGTCAAAATGGCGGGTGTATTTACCATCCACAACCTTTGAATTTGGTG	2785
QY	1861	CGCATCATATTGCCAAGCAATGAGATATTGTGATAAAGCAACAACCTGTCTCTAATACAT	1920
DB	2786	CACATCACATTCGGCAAGCAATGGCAAGTTGTGATAGCTACAACTGTTTCATATACGT	2845
QY	1921	ATTCAAAGGAAGTGTCCAGTCTATGGTGCATAGTTTCTCTCATCTTGGGAAATCTTATGGCA	1980
DB	2846	ATTCAAGGGAAGTGTCCAGCATGGTGTCTATTGSCCCTCACTTTTCCAAATTTACCGGTA	2905
QY	1981	TTCTCAATGGAATTGATTCGGATATATGGGATCCGTTACATGACAACTTTATCCCGGTCC	2040
DB	2906	TTCTGTAACGAATTGATTCAGATATTTGGGATCCATACAGTGACAAATTTATCCCGGTCC	2965
QY	2041	ACTACACTTGTGAGATGTGTGTTGAAGGCAAGAGGCTGCTAAGAGGCACTTCGACGACA	2100
DB	2966	ACTATACCTCTGAGATGTGTGTTGAGGGCAAGAGTGTCTGCCAAGAAGGCAATTTGCACAGA	3025
QY	2101	AGTTTGGGTTACAGCAAAATCGATGTCCCCGTCTAGGAAATCGTCACTCGCCTGACAGCCC	2160
DB	3026	GGCTTGSACTACAGCAACTGATACCCCTGTGTGTGGAATTAATCACTGCTGACAGTCC	3085
QY	2161	AAAAGGGGATCCACTGATCAAGATTCGGATTCACCGTTACCTCGAACCGGACGGACAGG	2220
DB	3086	AGAAGGGAATTCACCTTATCAAAACATGCAATTTATCGAACTCTTGAACGCAATGGCGAGG	3145
QY	2221	TGTTTTTGTCTGTTTACGCGCGGACTCTCGAATCCAAGCTGATTTTGTCAACCTCGGCA	2280
DB	3146	TGTTTTTACTAGGCTCAGCTCCAGATCATCGCATACAAGTGACTTTTCAACATTAGCTA	3205
QY	2281	ATACGCTCCACGGGTAAACCATCGGCAAGTGAAGCTTTCCTTGACTACGACGAGCCTC	2340
DB	3206	GTAACCTGCATGGCGAATACCAATGCTGTAAAGCTTTGTTAACTATGATGAGCCAC	3265
QY	2341	TCTCGCATCTGATATACGCTGGCTCTGACTTTCATCTTGGTCCCATCTATATTGAGCCTT	2400
DB	3266	TATCTCATTTGATTTATGCTGGTCCGACTTCATCTTGTTCCTTCATCTTTTGAACCTT	3325
QY	2401	CGCGCTTAACCTCAGCTCGTCCCATCGGTATGGAACCATCCGATGTGTCGCAAGACTG	2460
DB	3326	GTGGTTTTAAACCAGCTTACTGCTATGGTTATGGATCTATCCCAATAGTTTCGGAAACTG	3385
QY	2461	GAGGCTCTTCGCACACTGTCTTCGATGTGGCAATGACAAGGAACGAGCCGAGATCGAG	2520
DB	3386	GAGGCTTTTATGACACCGTTTTTGACGTGCAAGATGATAGGATCGAGCTCGAGAACAG	3445
QY	2521	GCCTTGAGCCCAACGGGTTTAGCTTTGACGAGCTGTATAGCAACGGTGTGTGACTACGCGC	2580
DB	3446	GTCTTTGAGCCAAACGGTTTCAGTTTTCGAAGGAGCTGACAGCAACGGTGTGGATTACGCC	3505
QY	2581	TGAAAGGGCGATCTC	2596
DB	3506	TTGACAGAGCGATCAC	3521

RESULT 7
ADCO7865
ID ADC07865 standard; DNA; 3032 BP.
XX
AC ADC07865;
XX
DT 18-DEC-2003 (first entry)

Rice DNA sequence Seq ID131 related to grain filling.
 plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
 wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
 gene; ds; plant.
 Oryza sativa.
 WO2003000905-A2.
 03-JAN-2003.
 21-JUN-2002; 2002WO-IB002450.
 22-JUN-2001; 2001US-0300112P.
 26-SEP-2001; 2001US-0325277P.
 20-DEC-2001; 2001US-0342327P.
 (SYGN) SYNGENTA PARTICIPATIONS AG.
 Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
 Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;
 WPI; 2003-229341/22.
 P-PSDB; ADC07866.
 New plant genes encoding polypeptides having an activity involved in or
 associated with the synthesis, metabolism or degradation of carbohydrates
 in the plant grain useful in generating plants having improved
 nutritional properties.
 Claim 2; SEQ ID NO 131; 130pp; English.
 This invention, in the area of plant biotechnology, relates to novel
 polynucleotides comprising a nucleotide sequence encoding a protein which
 is involved in or associated with the synthesis, metabolism or
 degradation of carbohydrates in the plant grain and the expression of
 which is up-regulated during grain filling. The plant is selected from
 corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
 sugarbeet, wheat, and rice. The invention may be useful for the
 improvement of protein, oil, starch, fibre and moisture content of the
 cereal grains. In addition, carbohydrate levels may be modified to a more
 desirable level using the present invention. The present sequence is a
 DNA sequence encoding a rice protein of the invention. Note: The sequence
 data for this patent did not form part of the printed specification, but
 was obtained in electronic format directly from WIPO at
 ftp.wipo.int/pub/publishedpct_sequences.
 Sequence 3032 BP: 873 A: 597 C: 735 G: 827 T; 0 U; 0 Other;

	Query Match	60.9%;	Score 1581.4;	DB 9;	Length 3032;
	Best Local Similarity	77.5%;	Pred. No. 0;		
	Matches 2048;	Conservative	0;	Mismatches 491;	Indels 102; Gaps 7;
Qy	1	AGCTTGCTGAAAAAATTTATTCGCTGGCAACAAGTTGTTTACTTATCCAGATGATATGA	60		
Db	323	AACVTGCTGCCAGATTGTTTCATGGGTAAACAGCTTTTCGTTTTCCAGAGGCAGTGA	382		
Qy	61	AAGCTGATTCAACAATTGATCTCTATTTCATTCGTGATCTATCAGCTGTGGCCAAATGAGC	120		
Db	383	AGGCTAATTCGACAATTGATGTATATTGTAATCGTAACCTATCGCTTTTGCGGAATGAGC	442		
Qy	121	CTGATGTACTTATCAAGGAGCATTCAATGGTGGAAAGTGAGATTTTTCACTCAAAAAT	180		
Db	443	CTGATGTCCCATCAAGAGGAGCATTCATAGTTGAGATGAGGGCCCTTACCGAAGAC	502		
Qy	181	TGCAACAAGAGCGAGCTGGCAGGGGACTGGTGGTCTGCAAACTATACATTCCTTAAGCAGG	240		
Db	503	TGCACAGCTGTAATTGAGTGGGATTTGGTGGTCTTGCAAACTGCATACCCAGGAGAG	562		

QY 241 CATACAGATGGACTTGTGTTTAAACGACACACGGTATGATAAATAACAATA 300
Db 563 CTTATAGATTAGACTTGTGTTCTCAATGGTCGTTAGTCTATGATAACAATGATAGTA 622
QY 301 ATGATTTGCGTATACAAATAGAAAGACACCAATGGATGAAATTTATTTGAGATTTCTTGG 360
Db 623 ATGATTTGCGTATACAAATAGAAAGTACAAATGGATGAAATTTCTTTGAGGAGTTCTTGG 682
QY 361 CTGAAGAAAGCAACGAGAACTTGAGAACCTTGCAAAATGAGAGAGCTGAAAGAGAGAC 420
Db 683 TTGAAGAAAGAAAGAGAACTTGAGAGAGTTGCCACTGAAGAGAGCTGAAAGAGAGAGGC 742
QY 421 AAACGTGATGACGCGCGGAATGAGAGAGAAAGAGGCGGAGATGAAAGCTGACAGAGGTAC 480
Db 743 ATGCTGAAGAGCAGCAGCGAATGGAGAAACAAAGGGCTGCAGAACAGCTGCCAGAGAAC 802
QY 481 AAGCAAGGTTGAGGTAGACGACGAGAAAGAAATAAATTTGCAATGTATTTGGGTTAGCCA 540
Db 803 AGGCTAAGAGGAGATAGAGTTGAAGAGAAACAAATTTGCAAAATCTCTTGAGTTACGCCA 862
QY 541 GAGCTCCTGTTGATTAATTTATGTTAGTACATTTAGGCCCATCAGACTGGACAGAGGCTACTG 600
Db 863 GAACACATGTTGATAATTTGTCGACATAGAGCGCTAGCACATATAGACAAAGGGGACACTG 922
QY 601 TCAGATGTTATTAACATAAATCAAGACCTCTAGTTTCAGTACTGAGATATGGATGC 660
Db 923 TCAGATTTGACTATACAGAAATCAAGGCGCTTATGCAATGACTGAGATCTGGATGC 982
QY 661 ATGCTGGCTATAACAAATGGATGATGAGTCTCTTTTGTGTAAGGCTGTTTCATCATC 720
Db 983 ATGCTGGTTGCAATAGTTGAGTCTGATGAGTCTCTATTTGTTGAAGACTTGTTCGAATGTG 1042
QY 721 ATGCAAGATTTGATGTTGTTGTTGAGATGTTGTCGTCCTGGAAGACATATGAT 780
Db 1043 ATGCAAGAAATGGTGGTGGTATGC-----TAATGCCCTGAAAGGCCCTTGTGAT 1094
QY 781 TGGACTGGGTTTTGCTGACGGGCCACAGGAGTGCAGAGAAATTATGACAAACAATGGAG 840
Db 1095 TGGACTGGGTTTTGCTGACGGGCCACCTGGAATGACAGAAATTATGACAAACAATGGTC 1154
QY 841 GACATGATTTTCATGCTACCTTCCAAATAACATGACTGAGAGAGAGATTTGATGAGAG 900
Db 1155 GACAAGATTTTCATGCTATTTCTCCAAATGCTGACTTAACAGAAATATTTGGGTTGAAG 1214
QY 901 AAGACAAAGGATCTATACAGGCTTCAACAGAGAGAGAGAGAGAGGAGGAGGCTATTA 960
Db 1215 AGGAAACTGTATCTATACAGGCTTCTCCAGAGATCAGAGAACGGGAGGAGGCTATTA 1274
QY 961 AAAGGAGGCTGAGAGAAATGCAAAATGAAAGCTGAGATGAAGGAAAGAACTATGAGAA 1020
Db 1275 A-----AATAAGAAATCTGAGATGAAGGAAAGAACTATGAGAA 1313
QY 1021 TGTTCCTGGTTCTCAGAAACACATGTTTTCACCGAACCACTTGAATATACATGCTGAA 1080
Db 1314 TGTTCCTGTTCTCAGAAACACATGTTTTCATCTGAACCACTTGAATATGCTGCTGAA 1373
QY 1081 CTACTATTGATGCTTTATATATCTTCTAATACAGTTCTTAACGAAAGCCAGAGGTTT 1140
Db 1374 CAACGTGAGATTTCTATATATCTTCTAATACGCTGCTGATGAGAAAGCCAGAGGTTT 1433
QY 1141 GGTTCGATGTTTCTTAAATCGTTGGATGTATPCCAGGTGGGTTGTGCCACTCAGAAAGA 1200
Db 1434 GGTTCGATGTTTCTTAAACGATGGATCTCCAAAGTGGTGTTCACCCCAAGAAAGA 1493
QY 1201 TGGTACAGAGAGAAATGGTTACACCTTAAGCAACAGTTTA-CGTTCCAGGATGCC 1259
Db 1494 TGGTGAAGAACAGAGATGGTTGCTACTTAAAGAGCAGAGTTAGTGTTCATCGGATGCT 1553
QY 1260 TATATGATGAGCTTCGTTTTCTCGAGTTCAGAAAGAGGTTGAAATTTATGATAACAGAAAT 1319
Db 1554 TATAATGATGAGCTTTGTTTTCTCGAGTTCGAAAGAGGTTGGAAATCTATGACAAAGGAAT 1613
QY 1320 GGGTTAGACTATCATATCTCTGTTTTTGGTGCATATTTGCAAGGAAACCACTATGACAT 1379

Db 1614 GGGACAGACTATCATATCTCTGTTTCCATGCAAGAGGAGCTCCCATTCATAT 1673
QY 1380 GTCCACATTTGCTGTTGAGATGGACCAATCGAAAGTTGGAGGTTGTTGATGTTGTC 1439
Db 1674 GTCCATATAGCGTTGAGATGGACCCATTCGAAAGTTGGAGGCTTGTGACGTTGTC 1733
QY 1440 ACTAGTCTTTTCAGTCTCTGTCGAAGATTTAGGACACAATGTGGAGGTTATTTCTTCCAAAG 1499
Db 1734 ACNAGTCTTTTCAGTCTCAATTCNAGATTTAGGCCATCATGTTGAGGTTATTTCTCCGAA 1793
QY 1500 TAGCGTTGCTTGAATCTAAGCAATGTCAAGATCTACAAATCCATCAGAGTTTCTTGG 1559
Db 1794 TATAATTTTATGATCAATCAAGCAATGTGAAGATTTGCATGTACGTCAAAAGCTTTCTTTG 1853
QY 1560 GGTGGTTCTGMAATAATGTGTGGCTGAGTCTGAGAGGCTTTGTGTTACTTCTTGG 1619
Db 1854 GGTGGTACAGAAATTAAGTGTGTTTGGACTAGTTGAAGACCTGCTGTTTACTTCTTGG 1913
QY 1620 GAACCTCAAAATGGGATGTTTGGAGTCCGATATGTATATGGCAGGACGATGACCGCGA 1679
Db 1914 GAACCTCAAAATGG-----GTATATGGAGGGAACGATGCTGGCAGA 1954
QY 1680 TTTGGTCTTTCTGTCGTTCTGCTCTAGAGTTTCTCTCCAAAGTGGATCTTCTCCGAA 1739
Db 1955 TTTGGTCTTTCTGTCGATCTGCTCTAGAGTCTCTCTCTCAGAGTGGATCTTCTCCAT 2014
QY 1740 ATAAATCAATTTGCCATGATTTGGTCAAGTCTCTGTTGCTGCTGCTACACAAGGAAACATC 1799
Db 2015 ATAAATCACTTGCCATGATTTGGTCAAGTGCACAGTTGCTGCTGCTATACAGGAAACAT 2074
QY 1800 GCGAAGTCTAGCTTGGCAACGCGGCTGTTTACCACATCCACATCTTGAATTTGGA 1859
Db 2075 GCAGATCCAGTTGGCAACTGCCCGGATTAATTTACCATCCATATCTTGAATTTGGA 2134
QY 1860 GCGCATCATATTTGGCAAGCAATGAGATATTTGTAAGAGCAACATGCTCTTAATACA 1919
Db 2135 GCATTTTATTTGMAAGCAATGACATCTGCGACAAAGCCCAAC-----TACG 2185
QY 1920 TATTCAAAGAGTGTGAGTCTGAGTCCATGTTGCTCTCTCTCTGTTGGAATTTCTATGGC 1979
Db 2186 TATTCAAAGAGTGTGAGTCTGAGTCCATGTTGCTCTCTCTCTCTGTTGGAATTTCTATGGA 2245
QY 1980 ATTCTCAATGGAATTTGATCCGGATATATGGATCCGTACAATGCAACTTTATCCCGGT 2039
Db 2246 ATTCTCAATGGAATTTGATCCAGATATCTGGATCCATATATACTGATAACTTCTCCCGGA 2305
QY 2040 CACT-----ACACTTGTGAA 2056
Db 2306 TAGTCATGATAGTGAATACATTTTATACAACTACCAGTCCATATATATCTCTGAAA 2365
QY 2057 TGTGTTTGAAGGCAAGAGGCTGTAAGAGGCACTGACAGAGAGTTTGGGTTACAGCA 2116
Db 2366 TGTGTTTGAAGGCAAGATGCTGCAAGAGAGCAATTCGACAGAGGTTTGGACTGACCA 2425
QY 2117 AATCGATGTCCTGCTGAGGATTCGTCACTCGCTGACGCCCAAGGGGATCCACCT 2176
Db 2426 GACTGATGTCCTGCTGAGGATTCGTCACTCGCTGACGCCCAAGGGGATTCACCT 2485
QY 2177 GATCAAGATGCGATTCACCGTACATCGACAGCAAGAGGAGGTTTGGTTC 2236
Db 2486 CATTAACATGCACTTTCATCGGACATGAAAGCAATGGACAGGTTTGGTTC 2545
QY 2237 AGCCCGGACTCTCGAATCCAAAGCTGATTTTGTCAAACCTGGCAATACGCTCCACGCGT 2296
Db 2546 AGCTCCAGATCTCGGATACAGAGTATTTCTGAGATTTGCTGATAGTCTTCTATGTTGA 2605
QY 2297 AAACCATGGCAAGTGGGTTTCTTTCAGCTACGACAGGCTCTCTCGCATCTGATATA 2356
Db 2606 AAACCATGGCAAGGTTAGACTATGTTTAACTTATGACAGGCTCTCTCACACCTGATATA 2665
QY 2357 CGTGGCTCTGACATTCATCTGTTGCCATCTATATTTGAGGCTTGGCGCTTAACTCAGCT 2416

Db 2666 TGTGGCTCTGACTTCATCCCTGTTCCATCCATCTTTGAACCTTGGCTTGGACTCACT 2725

Qy 2417 CGTCGCCATGCGGTATGAACATCCCGATTGTGCGAAGACTGGAGGG-CTCTTGGACA 2475

Db 2726 TGTGGCATGCGTATGATCCATCCCTATTGTTGGAAACCGGAGGACTTTACGACA 2785

Qy 2476 CTGCTTTGATGTGACATGACATGACAGGACCGCCGAGATCGAGCCCTTGAGCCCAACG 2535

Db 2786 CTGTTTTCGAGTAGACCATGACAAAGACCGGCTCGAGTTCTAGGCTTTGACCAATG 2845

Qy 2536 GGTTTAGCTTTGACGAGCTGATGACCAACGCGTGTGACTTACGCGTGAACAGGCGGATCT 2595

Db 2846 GGTTCAGCTTTGATGAGCTGACTGATGTTGTTGATGTTAGCCCTGAAACAGAGCAAT 2905

Qy 2596 C 2596

Db 2906 C 2906

RESULT 8

AAAF61270

ID AAF61270 standard; cDNA; 4121 BP.

XX

AC AAF61270;

XX

DT 25-MAY-2001 (first entry)

XX

DE Maize starch synthase protein encoding cDNA.

XX

XX Starch synthesis; starch synthase; maize; transgenic plant; nutrition;

KW modified starch; starch storage; ss.

XX

OS Zea mays.

XX

FH Key

FT 442..3954

FT /*tag= a

FT /product= "starch synthesis associated protein"

XX

PN DE19937348-A1.

XX

XX 22-FEB-2001.

XX

PF 11-AUG-1999; 99DE-01037348.

XX

PR 11-AUG-1999; 99DE-01037348.

XX

PA (AVET) AVENTIS CROPS SCIENCE GMBH.

XX

PI Froberg C;

XX

DR WPI; 2001-236028/25.

DR P-PSDB; AAB70781.

XX

XX New nucleic acid encoding a starch synthase isoform from maize, used to

PT produce recombinant plants that produce starch with modified properties.

XX

PS Claim 1b; Page 19-26; 32pp; German.

XX

CC This invention describes a novel nucleic acid (I) encoding a protein

CC (II), or its active fragments, with starch synthase (SS) activity

CC encoding a 1170 residue amino acid sequence (S2), comprising a 4121 base

CC pair sequence (S1), both fully defined in the specification, or its

CC complement, or containing the coding region of the cDNA insert in plasmid

CC IR65/87 (DSM 12970) or its complement. The invention also describes (1)

CC vector containing (I); (2) host cell, or transgenic plant cell, that

CC contains (I) or the vector of (1), or is derived from such a cell; (3)

CC (II), or its active fragments, encoded by (I); (4) production of (II), or

CC its active fragments, by culturing cells of (2); (5) plant containing

CC transgenic cells of (2), and their replicative material; (6) production

CC of the plants of (5); (7) starch produced by the plant cells of (2) or

CC the plants of (5), or their replicative material; and (8) production of

CC modified starch by extraction from the plant cells of (2) or the plants

CC of (5), or their starch-storing parts. (I) is used to prepare transgenic

CC plants (specifically maize) that have reduced or increased SS activity,

CC resulting in formation of starch with different chemical and/or physical,

CC and functional, properties, particularly altered viscosity and gel-

CC forming properties. Fragments of (I) can also be used as probes to

CC isolate related sequences from other organisms, also as antisense

CC inhibitors of SS activity. The starch produced by the transgenic plants

CC is useful for all usual nutritional and non-nutritional applications.

CC Modified starch may be better suited to particular applications

XX

SQ Sequence 4121 BP; 1180 A; 829 C; 1119 G; 993 T; 0 U; 0 Other;

Query Match 57.8%; Score 1500.4; DB 5; Length 4121;

Best Local Similarity 74.4%; Pred. No. 0;

Matches 1934; Conservative 0; Mismatches 601; Indels 63; Gaps 1;

Qy 1 AGCTTGCTGAAGAAATATTCGCTGGAAACAAGTGTCTTACCTTATCCAGATGATTTGA 60

Db 1298 AGCTTGCTGATGAGAAATATTCGACTGGGAACAACCTGTTTGTTCCTCGAAGTAGTGA 1357

Qy 61 AAGCTGATTCACACATTCATCTCTATTTCAATCGTGATCTATCAGCTGTGGCAATGAGC 120

Db 1358 AGGCTGATTCGATGATTCATCTTACTTAACCGCAGCATGTCGCGCTTAGTAGTGT 1417

Qy 121 CTGATGTACTTATCAAGGAGCAATCAATGGGTGGAAGTGGAGATTTTTCACGAAAAAT 180

Db 1418 CCGAGCTTTTGTAAAGGAGCAATCAATGGTTGGAGATGGAACCGTTTTCACCTGAAACAA 1477

Qy 181 TGCACAAGAGCAGCTGGCAGGGGACTGGTGTGCTGCAAACTATACATCTCTAAGCAGG 240

Db 1478 TGCATAGAAGCGAATTAAGAGGGGATTTGGTGTGCTGCAAGCTCTACATCCCAAGCAGG 1537

Qy 241 CATACAGATGACATTTGTTTAAACGGACACACGCTATATGAAATAATAACAATA 300

Db 1538 CATACAGACTGACTTTGTTTAAACGGTGACACTGCTCTATGAAATACAAATCACA 1597

Qy 301 ATGATTTTCGTGATACAAATAGAAAGCACCATGGATGAAATTTATTTGAGGATTTCTTGG 360

Db 1598 ACGATTTTTCCTGGAAATAGAAAGTGACATAGATGAACACTCATTGGAGGACTTCTTGG 1657

Qy 361 CTGAAGAAAGCAACGAGAACTTGAGAACCTTGCACATGAGGAGCTGAAAGGAGGAGAC 420

Db 1658 TTGAAGAAAGCGAAAGGAACTCGAGAGCTTGTCTGCAAGAAAGCTGAAAGGAAAGAC 1717

Qy 421 AAACCTGATCAGCAGCGCGCAATGGAGAAAGAGGCGCCGACAGATAAGCTGACAGGCTAC 480

Db 1718 AAGCTGAGAGCGGACACAGAGAGAGAGAGAGAGGCGCGGATGGAGCTGACAGGSCAC 1777

Qy 481 AAGCCAAAGTTGAGGTAG 540

Db 1778 AAGCAAGGCTCGAGGTCGAGATGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1837

Qy 541 GAGCTCCTGTTGATTAATTTATGTTATGTTATGAGCCCATCAGACTGCAGAGAGGCTACTG 600

Db 1838 GCAGATATGCTGAGAACTTATGTTATGAGAACTTAACACCTACAGAGAGGAGAGAGAG 1897

Qy 601 TCAGATTGTATTATAACATAAACTCAAGACCTTAGTTCACAGTACTGAGATATGAGATGC 660

Db 1898 TTGATTTGCTATTAATAGAGCTCGAGTCACTATATGATACACTGAGATTTGGATGC 1957

Qy 661 ATGGTGGCTATAACAATGGATTGATGGACTCTCTTTTGTCTGAAAGGCTTTGTCATCATC 720

Db 1958 ATGGAGTTTATACAACTGGATTGATGGACTCTCAATAGCTGAAAGACTTGTCAAAATCTC 2017

Qy 721 ATGACAAAAGATTGTTGATTTGGTGTGTTTGCAGATGTTCTGCTGCTGCAAGCAATATGAT 780

Db 2018 ATGAAAAGGAGGCGGATTTGGTGTATGTAGAAGTTACATTACCTGAAGGCGCATTTGTGT 2077

Qy 781 TGGACTGGGTTTTTGTGTGACGGCCCAAGGAGTGCAGAGAAATATGACAAACATGGAG 840

Db 2078 TGGATTGGGTTTTTGTGTGATGGACCACTGGGAAATGCAAGGAATTTATGATACAAATGGAA 2137

Qy 841 GACATGATTTTTCATGCTCTCCCTTCCAAATAACATGACTGAGGAAGAGTATTGGATGGAAG 900

PN EP779363-A2.
 XX 18-JUN-1997.
 XX 11-DEC-1996; 96EP-00309004.
 XX 12-DEC-1995; 95GB-00025353.
 XX (NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
 XX Smith AM, Marshall J, Edwards EA, Martin CR;
 PI WPI; 1997-312737/29.
 XX P-PSDB; AAW17785.
 DR Soluble starch synthase - used to produce altered starch from
 DR commercially important plants, e.g. potato, rice, wheat, and maize.
 PT Claim 16; Page 18-24; 39pp; English.
 XX A composite cDNA sequence (AA178646) codes for a 100-140 kDa potato
 CC soluble starch synthase (AAW17785). The sequence was deduced from 2
 CC overlapping cDNA clones obtained from a tuber cDNA library by
 CC immunoscreening with antiserum raised against purified starch synthase.
 CC Starch synthase nucleic acids can be linked to a plant promoter, in sense
 CC or antisense direction, and used to alter starch characteristics in
 CC transgenic plants, esp. potato, tomato, rice, wheat, pearl cassava, sweet
 CC potato, barley, oat or maize. A novel altered starch, extracted from such
 CC transgenic plants, has a viscosity onset temperature that is reduced by
 CC at least 5 degC compared to starch from non-transformed plants. (Updated
 CC on 17-OCT-2003 to standardise OS field)
 XX SQ Sequence 4127 BP; 1282 A; 709 C; 977 G; 1159 T; 0 U; 0 Other;
 Query Match 46.4%; Score 1204.8; DB 2; Length 4127;
 Best Local Similarity 66.7%; Pred. No. 0;
 Matches 1735; Conservative 0; Mismatches 862; Indels 3; Gaps 1;
 2 GCTTGTGAAAAAATTTTCGCTGGGAAACAAGTTGTTTACTATCCAGATGATTGAA 61
 1111 GCTTGTGAAAAAATTTTATTCGAGGATTCAGATTATTTTGTTCAGAGTTGTA 1170
 62 AGCTGATTCACAAATGATCTCTATTCTCATCTGATCTATCAGCTGTCGCAATGAGCC 121
 1171 ACCTGATGAGATGTCAGATATTTCTTAACAGAGTCTTCCACTTTGAAGATGATC 1230
 122 TGATGTACTTATCAAGGAGCAATTCATGCTGGAGTGGAGATTTTCTACTGAAAAAT 181
 1231 TGATGCTTGAATATGGAGCTTTTATGATGAGTGGCGCTATAGGTCTTTTACTACAGGCT 1290
 182 GCACAGAGCGAGCTGCGAGGAGCTGCTGCTGCTGCAAACTATACATCTCTAAGCAGGC 241
 1291 AACTGAGACTCATCTCAATGGAGATTTGGTGTCTTGAAGATCCATGTTCCCAAGGAAGC 1350
 242 ATACAGATGCACTTCTGTTTTTAAACGACACACCGTATATGAAATTAATCAATAA 301
 1351 ATACAGGCTGATTTGTTTTTATATGACAGATGCTATGACACAAATGATGAAA 1410
 302 TGATTTCTGATCAATATAGAAAGCACCATCGATGAAAAATTTATTCAGGATTTCTTGGC 361
 1411 TGACTTCAGTATACCTGTAAGAGTGTATGCAATCATTTGACTTTGAAAAATTTCTTGTCT 1470
 362 TGAAGAAAGCAACGAACTTTGAGAACTTGGCAATGAGGAAGCTGAAAGGAGGACACA 421
 1471 TGAGGAGAAATGGAGAGAACAGAGGAACTTTGTAAGAAACAAAGCTGAAAGAGAAAGCT 1530
 422 AACTGATGAGCAGCGGCAATGGAGGAGAAAGGCGCGACATAAAGCTGACAGGTACA 481
 1531 AGGAGAGAACAAAGACGAATAGAGCGAGAGAAAGCTGAATGGAAGCTGACAGGACACA 1590
 482 AGCCAAAGGTTGAGGTAGAGACGAAAGAAATTAATTTGCAATGATTTGGGTTTAGCCAG 541
 1591 AGCAAGGAGAGGCTGCAGAGAAAGAAAGATTTGCGAGAAATGATGTTAAAGCCAC 1650

QY 542 AGCTCCTGTTGATAATTTATGTTACATTCAGCCCATCAGACTGCAAGAGAGGCTACTGT 601
 DB 1651 GAAGACTCGTGAATATCACCCTGGTACATAGAGCCAGTGAATTTAAATCGGAGGACAGGT 1710
 QY 602 CAGATTGTATTATAACATAAACTCAAGACCTCTAGTTCAAGTACTGAGATATGATGCA 661
 DB 1711 CAGGTTATACTATACAAAAGTTAGGTCTCTCCCATGCTAAAGGACTTGTGGATCCA 1770
 QY 662 TGGTGGCTATACAAATTTGATGAGTACTCTCTTTGCTGGAAGGCTTGTTCATCATCA 721
 DB 1771 CGGAGGATATAATAATTCGAAAGGATGGTTGCTATTGTCAAAAAGCTTGTTAATCTGA 1830
 QY 722 TGACAAAGATTTGATTTGGTGGTTTTGCAGATGTTGCTGCTCGCTGAAAGCAATATGTATT 781
 DB 1831 GAGAAATAGATGGTGAATGGTGGTATACAGAGGTTGTTATTCTCTGATCAGGCACTTTCTT 1890
 QY 782 GGACTGGGTTTTTGTGACGGCCCAACAGGAGTGCAGGAATTTATGACAAATGGAGG 841
 DB 1891 GGATTTGGGTTTTTGTGATGGTCCACCCCAAGCATGCCATTTGCTTATGATAACAATCACCG 1950
 QY 842 ACATGATTTTCATGCTACCCCTTCCAAATAACATGACTGAGGAGAGATTTGATGGAAGA 901
 DB 1951 CCAGACTTCCATGCCATTTGCCCAACCAATCCGGAGGAATTAATTTGGTTGAGGA 2010
 QY 902 AGAACAAAGGATCTATACAAGGCTTCAACAAGAGAGGAGGAGGAGGAGGCTATTAA 961
 DB 2011 AGAACATCAGATCTTTAGACACTTCAGAGGAGAGAGAGGCTTAGAGAGCGCTATGCG 2070
 QY 962 AAGGAGGCTGAGAGAAATGCAAAAATGAAAGTGAAGTGAAGGAGGAGGAGGCTATGAAAT 1021
 DB 2071 TGCTAAGGTTGAAAAAACAACGACTTCTGAAAACTGAAACAAAGGAGGAGGCTATGAAATC 2130
 QY 1022 GTTCTGGTTTTCTCAGAAACACATTTGTTTACACCGAACCATTTGAAATACATCTGCAAC 1081
 DB 2131 ATTTTCTACTGTCTCAGAGCATGTAGTATATCTAGAACTCTTTGATATCCAGCTGGAAG 2190
 QY 1082 TACTATTGATGTGCTTTATAATCCCTTCTAATACAGTTCTAACTGGAAGGAGGAGGCTTTG 1141
 DB 2191 CAGGCTCAGTTTACTATTAATCCCGCCCATACAGTACTTAATGGTAAACCTGAAATTTG 2250
 QY 1142 GTTTCGATGTTCTTTTAAATCGTTGGATGATCCAGTGGGGTGTTCACCTCAGAGAT 1201
 DB 2251 GTTCAGATGTTTCAATTAATCGCTGGACTCACCGCTGGGTCCATTTGCCACCTCAGAAAT 2310
 QY 1202 GGTAACAGAGAAATGGTTTACACCTAAAGCAACAGTTTACGTTCCAGGATGCTA 1361
 DB 2311 GTCGCTGTGAAAAATGGCACCCATGTCCAGAGCACTGTGAAGGTTCCATTTGATGATGATA 2370
 QY 1262 TATGATGGACTTCGTTTTCTCGGAGTCAAGAGAGGTTGGAATTTATGATAACAGAAATGG 1321
 DB 2371 TATGATGGATTTTGATTTTCCAGAGAGAGAGATGGTGGGATTTTGGACAAATAGAGCGG 2430
 QY 1322 GTTAGACTATCATTTCTGTTTTGGGTCAATTCGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 1381
 DB 2431 AATGAGCTATCATACCTGTTTGGAGGAGTCCGCTAAAGAAACCTCCCAATGATATGT 2490
 QY 1382 CCATTTGCTGTTGAGATGGCAACCAATCGCAAGGTTGGAGGCTTTGGTGTGATGTTGTCAC 1441
 DB 2491 CCATTTGCTGTTGAGATGGCAACCAATTCGAAAGGTTGGAGGAGGAGGAGGAGGAGGAGG 2550
 QY 1442 TAGTCTTTTACGCTGCTGTCAGAGATTTAGGACAAATGTGGAGGTTATTTCTTCCAAAGTA 1501
 DB 2551 TAGTCTTTCCGCTGCTGTTCAAGATTTAAACCAATATGTGATATTTATCTTACCTAAGTA 2610
 QY 1502 CGGTGCTTCAATCTAAGCAATGTCAAGATCTCAAAATCCATCAGAGGTTTCTTGGGG 1561
 DB 2611 TGACTGTTTCAAGATGAATTAATGTGAAGGACTTTCGGTTTTTCAAAAAAATCTACTTTTGGGG 2670
 QY 1562 TGGTCTGAATTAATGTTGGGCTGGAGTGTAGTGGAGGCTTTGCTTTTACTTCTCTGGA 1621
 DB 2671 TGGGACTGAAATAAAGTATGGTTTGGAAAGGTTGGAAAGGCTCTCGGTCTATTTTTTGGGA 2730

1622	ACCTCAAAATGGGATGTTGGAGTCCGGATATGTATATG---GCAGGGACGATGACCGCGC	1678
1679	ATTTGGCTTTCTCGTTCGTCTAGAGTTTCTCTCCAAAGTGGATCTTCTTCGGAA	1738
1739	CATAATCATATGGCCATGATTGGTCAAGTGCCTCTTGCTTGGCTGGCTTACAAAGGAAACTA	1798
1799	CGCGAAGTCTAGCTTTGGCAACCGCACGGGTGGTATTACCAATCCACAATCTTGAATTTGG	1859
1859	ACGCATCATATTTGGCAAGCAATGAGATATTGTGATTAAGCAACAACTGCTCTTAATAC	1918
1918	TATCATTTCAATGCCATGATTGGTCTAGTGTCTCTGTTGGCTCTTTTAGGAACAATA	1978
1978	GGCAGATCTCATTTGGGAGAGCAATGACTAACCGACACAAGACTCAACAGATTTCACCAAC	2038
2038	ATATTCAAAGGAAGTGTCAAGTTCATGGTCCCATAGTTTCTCTCATCTTGGAAATTTCTATGG	2098
2098	TTACTCACAGGAGGTCTCTGGAACCCCTGTAATTTGGGCTTCACTTCAAGTTCATATGG	2158
2158	CATTCTCAATGGAAATTTGATCCGGATATATGGGATCCGTACAATGACAACTTTATCCCGGT	2218
2218	TATAGTGAATGGGATTTGACCCAGATATTTGGGATCCTTTAAACGATTAAGTTCATTCCGAT	2278
2278	CCACTACATTTGTGAAATTTGGTTGAAGCAAGAGGGCTGCTAAGAGGGCACTGCAGCA	2338
2338	TCGGTACACTTCAGAAAAAGTTTGTTCAGGGCAAAACAGCAGCCAAAGGAAGCTTTGACGG	2398
2398	GAAATTTGGGTTACAGCAATCGATGCTCCCGTCGTAGGAATCGTCACCTCGCTGACAGC	2458
2458	AAACCTTTGGACTGAACAGGCTGACCTCTCTTTGGTAGGAATTAATCAGCGCTTAATCTCA	2518
2518	CCAAAGGGGATCCACCTGATCAAGCATGCGATTCACCGTACACTCGAATCGGAACGGACA	2578
2578	CAGAAAGGAATCCACCTCATTAACATGCTATTTGGCGCACCTTGGAAACGGAAACGGACA	2638
2638	GGTGGTTTGGCTTGGTTACGGCGGCACTCTCGAATCCAGAGTGAATTTGTCAACCTGGC	2698
2698	GGTAGTCTTGTCTGGTTCTCTCTGATCCAGGTCACAAAACAAATTTGTAAATTTGGC	2758
2758	GAATACGCTCCACGGCGTAAACCATGGGCAAGTGAGGCTTTCTTTCACCTTACGACGAGCC	2818
2818	AAATCAATTTGCATCCCAATTAATGACCGCGCACGACTCTGTCTAACATATGACGAGCC	2878
2878	TCCTCCGACTGATATACGCTGGCTGATCACTTCTGGTCCCATCTATATTTAGGCC	2938
2938	ACTTTCTCACCTGATATATGCTGGTGTGATTTAATTTCTAGTTCTTCAATATTTGAGCC	2998
2998	TTGGCGCTTAACACTCAGCTCGTCCGATCGGTATGGAAACCATCCCGAATTTCTCCGCAAGAC	3058
3058	ATGTGGACTTAACAACTTAACCGCTATGAGATATGGTTCAATTTCCAGTCTGGTGAAC	3118
3118	TGGAGGCTCTTCGACACTGCTTTCCGATGTGGACAATGACAAGGAAACGAGCCCGAGATCG	3178
3178	TTGAGGACTTTATGATACTGATTTGATTTGACCATGACAAGAGAGAGCAACAACAGTG	3238
3238	AGGCTTTGAGCCCAACGGTTTACGTTTGAAGGAGCTGATAGCAACCGGTGTGACTACGC	3298
3298	TGGTCTTTGAACCAATGGAATTCAGCTTTGATGGAGCAGATGCTGGCGGAGTTGATTATGC	3358
3358	GCTGAACAGGGCGATCTCAG	2598
3359	TCTGAATAGAGCTCTCTCTG	3710

AC	ADA68321;	
XX	20-NOV-2003 (first entry)	
XX	Arabidopsis thaliana gene, SEQ ID 816.	
XX	plant; bacterial infection; fungal infection; viral infection; ds.	
KW		
XX	Arabidopsis thaliana.	
OS	WO200300898-A1.	
PN	03-JAN-2003.	
PD	22-JUN-2001; 2001WO-IB001105.	
XX	22-JUN-2001; 2001WO-IB001105.	
XX	(SYGN) SYNGENTA PARTICIPATIONS AG.	
PA	Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;	
XX	Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;	
PI	WPI; 2003-175290/17.	
DR	Identifying at least one gene involved in plant resistance or response to	
XX	pathogenic infection for conferring resistance or tolerance to a plant to	
PT	bacterial, fungal or viral infection by determining or detecting plant	
PT	gene expression.	
XX	Claim 6; SEQ ID NO 816; 899pp; English.	
PS	The present invention relates to a method (M1) for identifying genes	
XX	involved in plant resistance or response to pathogenic infection. M1	
CC	comprises identifying a gene whose expression is significantly altered in	
CC	the incompatible interaction of plant gene expression relative to	
CC	expression of the gene in an uninfected plant in a mutant plant that	
CC	does not express a gene associated with response to pathogenic infection,	
CC	or in a corresponding incompatible or compatible interaction. (M1) is	
CC	useful for conferring resistance to resistance or tolerance to a plant to	
CC	bacterial, fungal or viral infection. The present sequence was used to	
CC	illustrate the invention.	
XX	Sequence 3078 BP; 946 A; 535 C; 763 G; 834 T; 0 U; 0 Other;	
SQ		
Query Match 43.9%; Score 1141.2; DB 7; Length 3078;		
Best Local Similarity 65.7%; Pred. No. 0;		
Matches 1719; Conservative 0; Mismatches 878; Indels 21; Gaps 3		
QY	2 GCTTGCTCAAAAATTTATTCGCTGGGAACAAGTGTGTTACTTATCCAGATGATTGAA 61	
DB	342 GCTTGCAAGCGAAATTTGGCGAGGTGATAGAAATTTGTGTATCCCGTTATTGTGAA 401	
QY	62 AGCTGATTCACAAATGATCTCTATTTCAATCGTGATCTATCAGCTGTGGCAATGAGCC 121	
DB	402 ACCTGATGAACACATAGAAAGTGTTCCTCAACGGAATCTGTGACTGTGAATAAGAAC 461	
QY	122 TGATGTACTTATCAAGAGCATTCATGAGTGGTGAAGTGGAGATTTTTCACGTGAAAATT 181	
DB	462 CGATGTTTTGATCATGGGGCGTTTAAACGAATGGAGATGGAAGTCTTTTCAAGAGGAT 521	
QY	182 GCACAAAGACGAGCTGGCAGGGGACTGTGTGCTGTGCAAACTATACATCTCTAAGCAGC 241	
DB	522 GGAAAGACCTGGATCCCATGAAGATTTGTTGTGATCTCTCTTATATATATATATATAT 581	
QY	242 ATACAGATGACTTGTGTGTTTTTAAACGACACACGCGTATATGAAATATATAACAATA 301	
DB	582 GTAAGAATGAGACTTCGTTGTTTTTCAATGGGCAAGTGTATATGACACAAATGACTCAA 641	
QY	302 TGATTTTCGTGATACAAATAGAAAGCACCATGGATGAAATTTATTTGAGATTTCTTGCC 361	
DB	642 AGATTTTGTGTAGAGATAAAGGTTGGGATGATTAAGTTGACTTTGAGAAATTTCTTCT 701	

362	QY	TGAAGAAAGCAACGAGAACTTGGAACTTTGCAATTCAGGAAGCTGAAAGGAGGAGACA	421
702	Db	AGAGAGAGAACTGGCAGAGCAAGAGAACTTAGCCAAAGGAGAGCTGAGAGGAGAGGCA	761
422	QY	AACTGATGAGCAGCGCGAAATGGAGGAAGAAGGGCCGACGATAAAGCTGACAGGTACA	481
762	Db	AAAGAGAGAGAGAGAAATCGAAGCTCAAAGGCTGCAATTGAAGCTGATAGAGACA	821
482	QY	AGCCAAAGGTTGAGGTAGAGACGAAGAAGATPAAATTTGTGCAATGTATTTGGGTTTGGCCAG	541
822	Db	AGCAAAAGCGCGAGACTCAGAGAGACGTGAATTCGCTTCAACCGGCTATTAAGAAGCTGT	881
542	QY	AGCTCCCTGTTGATATTTATGCTACATTTAGGCCCATCAGACTCGCAAGAGGCTACTGT	601
882	Db	AGTCTCGGCTGAGATGTTTGGTACATTCAGCCGAGTGTATTTCAAGGCTGAAGATACAGT	941
602	QY	CAGATTTGATTAATTAACATAAACTCAAGACCTCTAGTTCCAGTACTGAGATATGGATGCA	661
942	Db	GAAGCTATATTAATAAAGGTCAGGTCCTCTGACTAATTTCCAAGAACTGTGGTTACA	1001
662	QY	TGTTGCTATACAANTGGATTCAGTGAGCTCTCTTTGCTGTAAGGCTTGTTCATCATCA	721
1002	Db	TGGAGGGTTTAAATTTGGTTGATGGATATCTATCGTTGTAAAGCTTGTATATGCTGA	1061
722	QY	TGCAAAAGATTGTG-----ATTGGTGGTTTGAGATGTTGTCTGCTCTGA	766
1062	Db	GTTTAAAGGATGTTGATCCAAAGACGGAAATTTGGTGGTTTCGCTGAAGTTGTAGTCCCTGG	1121
767	QY	AAGAAACATATGATATGGACTGGGTTTTTGTGACGGCCACAGGGAGTGCAGGAATTA	826
1122	Db	CGGTGCACTAGTCAATTTGACTTGGGTCCTTGTGATGGACCACTTAAAGGAGCGTTTCTGT	1181
827	QY	TGACAAANTGGAGGACATGATTTTCATGCTACCTTCCAAATTAACATGACTGAGGAAGA	886
1182	Db	TGCAATAATGGTTTACAGACTTCCAGCACTTGTCTCTCAAACTTCTCTGAAGAATCT	1241
887	QY	GTATTGGATGGAGAAGAAACAAAGGATCTATAAAGGCTTCAACAGAGAGAGGGAAG	946
1242	Db	TTACTGGTTAGAGGAAGAAATATGATTTTGAAGAACTTCAGGAGGATAGGCGGTTAA	1301
947	QY	GGAGGAGGCTATTAAAGGAAGGCTGAGAGAAATGCAAAATGCAAGCTGAGATGAAGA	1006
1302	Db	AGAGGAAGTTATGCGTCCAGATGGAAAGAACAGCTCGCTTGAAGCTTGAACCTTAGGA	1361
1007	QY	AAAGACTATGAAATGTTCTCTGGTTTCTCAGAAACACATTTGTTTACACGAAACCACTGA	1066
1362	Db	AAGAACCTGAAAAGTTTCTGCTATCCAGAAAGACGTGGTTTACACGAGCCTCTAGA	1421
1067	QY	AATACATGCTCGAACTACTATGATGTCGTTTATATCTTCTAATACAGTTCCTACTCG	1126
1422	Db	GATTCAGCAGAAACCCGTGTGACTGTATTTGTACAATCCTGCAACACGGTTTGAATGG	1481
1127	QY	AAAGCCAGAGTTTGGTTTCGATGTTCTTTTAAATCGTTGGATGTATCCAGCTGGGGTGT	1186
1482	Db	AAAACCTGAAGTTTGGTTTAGAGGCTCTTTTAAATCGTTTGAAGTCTACCGCTTGGCCCTTT	1541
1187	QY	GCACCTCAGAGATGGTACAGCAGAGAAATG---GTTCAACCTAAAACACAGTTTA	1243
1542	Db	GCACCTCAGAAATGGAGCAACAGATGATGAAGCTCAATGTGAAGACTACGGCTAA	1601
1244	QY	CGTCCACAGAGATGCTATATGATGGACTTCGTTTCTCGAGGTCAGAAAGGTGGAAT	1303
1602	Db	GGTCCCATTTGATGCTTACATGAGCACTTTGTGTTCTCTGAGAAAGAGGATGCGGAAT	1661
1304	QY	TTATGATAACAGAAATGGGTTAGACTATCATATTTCTGTTTGGGTCATTTGCAAAAGGA	1363
1662	Db	ATTGATATAAATAATGGTCTGGATTTACATTTACCAGTCGTGGGAGGTATTTCAAAGGA	1721
1364	QY	ACCACCTATGCAATTTGTCCACATTTGCTGTTGAGATGCAACAATTCGAAGAGTTTGAGG	1423
1722	Db	ACCACCATTTGCATTTGTTTCATATTTGCTGTTGAAATGGCAACCAATCGCAAAAGTTGGTG	1781
1424	QY	TCCTGGTGAATGTCACCTAGTCTTTTCCAGTCTGTGCAAGATTTAGGACACAATGTGGA	1483

1782	Db		CTAGTGAAGTGTGACATAGTCTATCTCGCGCTGTTCAAGAAATTAACCATATATGGGA	1841
1484	Qy		GGTTATTTCTCCAAAGTAGCGGTGGTGGATCTTAAGCAATGTCAAGAAATCTACAAATCCA	1543
1842	Db		TATAGTTTTTCCAAAGTAGTATGTCATTAAGACACAATTTGTGAAGGACTTGCAAATTTAA	1901
1544	Qy		TCAGAGTTTTTCTCGGGTGGTTCTGAAATAAATGCTGTGGCTGGAGCTAGTTCGAAGGCT	1603
1902	Db		CAGAAGCTATCATCTGGGAGGAACATGAATAAAGTTTGGCATGGAAAGTAGAAGGCT	1961
1604	Qy		TTGTGTTTATCTCTCGGAACCTCAAAATGGGAAGTTTGGAGTCGGATATGTATATGGCAG	1663
1962	Db		TTCGGTTTACTTCTTAGATCCACAAAATGGATGTCTCAGCGAGATGTGTTTACGGTTG	2021
1664	Qy	----	GGACGATGACCGCGGATTTGGCTTCTTCTGTCTGTCTGTCTCTAGAGTTTCTCTCCCA	1720
2022	Db		TGCAGATGATGACGAGAAGATTCGGTTTCTTCTGTCTATCGGCTCTTGAATTTCTTCTCA	2081
1721	Qy		AAGTGGATCTTCTCCGAAACATAATACATTCGCATGATTTGGTCAAGTGCTCCGTGTTGCC	1780
2082	Db		AGAGGTTTCCATCCAGACAATCTTTCACCTGTCTAGTGGTCTAGTGTCTCGGTTCTCATG	2141
1781	Qy		GCTACACAAGGAAAACTACCGGAAGTCTTAGCTTGGCAACGACCGGTGTATTCACCAT	1840
2142	Db		GTTATTCAGGATCATTTACACACAGTACGGTTTAATTTAAAAACCGTATTTGCTTCACAA	2201
1841	Qy		CCCAAACTTTGAATTTGGAGCGCATCATATTGGCAAGCAATGAGATATTTGTGATAAAGC	1900
2202	Db		TCATAATTTTGGAAATTTGGAGCGAATGCCATTTGTAAGCAATGACATTTGCAGACAAAGC	2261
1901	Qy		AACAACCTGTCTTAATACATATTTCAAAGGAAGTGTACGTCATGTGTGCCATAGTTCCTCA	1960
2262	Db		CACAAAGGTTTCAACCACTTATGCTAAGGAAGTTGCTGGAAACTCTGTATCTCTGCACA	2321
1961	Qy		TCCTGGGAATTTATGGCAATTTCTCAATGGAATGATCCGGATATATGGATCCGTACAA	2020
2322	Db		TTTATACAAAATTTCAACGGAAATTAACACGGGAATGACCCAGATATATGGATCCATATA	2381
2021	Qy		TGACAACTTTATCCCGTCCACTACACTCTGTGAGAATGTGTTTGAAGGCAAGAGGCTGC	2080
2382	Db		CGATAACTTTATTTCCGGTACCTTATATCTTCAGAGAACGTTGTAGAGGCAAAAGAGCAGC	2441
2081	Qy		TAAAGGGCACTGCAGACGAAGTTTGGTTTACAGCAATCGATGTCCCCGTCTGTAGGAAT	2140
2442	Db		CAAGGAAGAAATGCAAAACAGGCTTGGACTTAAGAGTGCCGATTTTCCAGTAGTAGGAAT	2501
2141	Qy		CGTCACTCCGCTGACAGCCCAAAAGGGATCCACTCATCAAGCATCGCAATTCACCGTAC	2200
2502	Db		TATTACGGCTTTAACACACCCAGAAGGAATACATTTGATCAAGCACGTAATTTGGGGTAC	2561
2201	Qy		ACTTCGAAACGGAAACGACAGGTGGTTTTTGTGTGTTTCAGCGCCGGAATCTCGAATCCAGC	2260
2562	Db		CTTTGAAACGGAAATGACAGGTTGTCTTATTAGGTTTCAGCTCCAGATCCTCGGATCCAAA	2621
2261	Qy		TGATTTGTGTAACCTGGCGGAATACGCTCCAGCGGTAAACCATGGGCAAGTAGAGGCTTTC	2320
2622	Db		TGATTTGTGTAACCTTGGCAAAACCAATACATTTCTTCATGGTGAACCGGCTCGGCTTGT	2681
2321	Qy		CTTTGACCTACGAGGCTCTCTCGCATCTGATATAGCTGGCTCTGACTTCAATTCGTGT	2380
2682	Db		TCTAACCTTACGATGAACCTCTTTCCCATTTGATTTATGCTGGGCTGACITTTATTTCTGT	2741
2381	Qy		CCCATCTATTTTGGCCTTCGGCCTAACTCAGCTCGTCCCATGCGGTATATGSAACCAT	2440
2742	Db		ACCGTCGATTTTGAAGCCATGTGGAAGTACACAGCTCATAGCCATGATGATACGGCGCTGT	2801
2441	Qy		CCGATTTGTCGAGAGCTGGAGGCTCTCTGACACTGTCTTCGATGTGGACAATGACAA	2500
2802	Db		TCTGTGTGTGTGAAAACCTGGAGGACTCTTTTGATACGGTTTTTGTATGTGTGCCAGATA	2861
2501	Qy		GGAAACGAGCCCGAGATTCGAGGCTTTGAGCCCAACGGGTTTAGCTTTTGAACGAGTGTATG	2560

QY 1960 ATCTTGGAAATTCATGGCAATTCCTCAATGAATGATCCGGATATATGGGATCGGTACA 2019
Db 1271 ACCTTACAGATTCATGGTATAGTGAATGGATGACCCAGATATTTGGGATCCTTTAA 1330
QY 2020 ATGACAACTTTATCCCGTCCACTACACTTGTGGAATGTGGTTGAAGGCAAGGGCTG 2079
Db 1331 ACGATAGTTCAATCCGATTCGTACACTCAGAAAACGTTGTTGAAGGCAAAACAGCAG 1390
QY 2080 CTAAGAGGCACTGACAGCAAGTTTGGGTTTACAGCAATCGATGTCCTCGTGTAGAA 2139
Db 1391 CCAAGGAGCTTTGACGCGAAACCTTGGACTGAAACAGGCTGACCTTCTTTGGTAGGAA 1450
QY 2140 TCGTCACCTGCTGACAGCCCAAGAGGATCCACTGATCAAGCATCGGATTCACCGTA 2199
Db 1451 TTATCAGCGCTTAACTCACCAGAAAGGAATCCACTCATTAACATGCTATTTGGCGCA 1510
QY 2200 CACTCGAAGCAAGCAAGTGGTTTGTCTGGTTTCAGCGCGGACTCTCGAATCCCAAG 2259
Db 1511 CTTTGGAAAGCAAGCAAGTAGTCTTGGTTCTGCTCTGCTGATCCTAGGCTACAA 1570
QY 2260 CTGATTTTGTCAACCTGGCAATACGCTCCACGGGTAAACCATGGCAAGTGAGGCTTT 2319
Db 1571 ACGATTTTGTAAATTTGGCAATCAATTCGACTCCAAATATTAATGACCGCGCACGACTCT 1630
QY 2320 CTTGACCTACAGAGGCTCTCTGCACTCTGATATACGCTGGCTGTGACTTCATTTCTGG 2379
Db 1631 GTCTAACATATACAGAGGCACTTTCTCACTGATATATGCTGGTGTGATTTATTTCTAG 1690
QY 2380 TCCATCTATATTTGAGCTTGGCGCTCAACTCAGCTCGTCGCCATGCGGTATGGAACCA 2439
Db 1691 TTCCTTCATATTTGAGCCATGTGACTTAACCACTTACCGCTATGAGATATGTTCAA 1750
QY 2440 TCCGATTTGCCGAGAGCTGAGGAGCTCTCGACACTCTGCACTCTGTTGCAATGAGCA 2499
Db 1751 TTCCAGTCTGCTAAACTGGAGGACTTTATGATACTGTTATTTGATGTTGACCATGACA 1810
QY 2500 AGAAGGAGCCCGAGATCGAGGCTTGAAGCCCAAGGTTTACGTTGACGGAGCTGATA 2559
Db 1811 AAGAGAGAGCAACAGTGTGGTCTTGAACCAATGGATTCAGCTTTGATGAGCAGATG 1870
QY 2560 GCAACGGTGTGACTACGGCTGAACAGGGCGGATCTCAG 2598
Db 1871 CTGGCGGAGTTGATATGCTCTGAATAGAGCTCTCTCTG 1909
RESULT 12
AAC86416
XX AAC86416 standard; DNA; 2446 BP.
AC AAC86416;
XX
XX 01-MAR-2001 (first entry)
XX
XX Wheat starch synthase III gene fragment SEQ ID NO: 12.
DE
XX Wheat; starch synthase; SSII; SSIII; starch content; starch synthesis;
XX food product; adhesive; db.
XX
XX Triticum sp.
OS
XX WO200066745-A1.
PN
XX 09-NOV-2000.
PD
XX 28-APR-2000; 2000WO-AU000385.
XX PF
XX 29-APR-1999; 99AU-00000052.
XX PR
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (GOOD-) GOODMAN FIELDER LTD.
PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
XX
XX Morell M, Li Z, Rahman S, Appels R;
PI

XX WPI; 2000-647602/62.
DR Nucleic acid molecules encoding wheat starch synthase (WST)-I and WST-II,
XX useful in modifying plant starch content and/or composition.
PT Claim 1; Page 187-188; 211pp; English.
PS
XX The present invention relates to novel protein and coding sequences from
CC wheat. The proteins are wheat starch synthases, designated SSII and
CC SSIII. These can be used in the modification of plant starch content or
CC composition, and to screen plants to identify mutations which affect
CC starch content and composition. The starch can then be used in food
CC products, such as flour, and in films, coatings, adhesives, building
CC materials and packaging materials
XX
SQ Sequence 2446 BP; 780 A; 400 C; 624 G; 642 T; 0 U; 0 Other;
Query Match 19.3%; Score 501; DB 3; Length 2446;
Best Local Similarity 76.8%; Pred. No. 2.2e-137;
Matches 612; Conservative 0; Mismatches 185; Indels 0; Gaps 0;
QY 1 AGCTTGTCTGAAAAAATTTATTCGATGAGGAAACAAGCTGTTGTTTTCCAGAGGTAGTGA 1245
Db 1186 AACTCGCTGAGAAAAAATTTATTCGATGAGGAAACAAGCTGTTGTTTTCCAGAGGTAGTGA 1245
QY 61 AAGCTGATTCACAAATTCATCTTATTCATCGTGAATCATCAGCTGTGGCCAAATGAGC 120
Db 1246 AAGCTGATTCAGTATTCATCTTATTCATCGTGAATCATCAGCTGTGGCCAAATGAGC 1305
QY 121 CTGATGCTATTCATCAAGGAGCAATTCATGGGTGGAAGTGGAGATTTTTCATCTGAAAAAT 180
Db 1306 CCGATGTTGTCATCAAGGAGCAATTCATGGGTGGAAGTGGAGCTTTTTCATCTGAAAAAT 1365
QY 181 TCACAAGAGCGAGCTGGCAGGGAGCTGGTGTGCTGCAAACTATACATTCCTTAAGCAGG 240
Db 1366 TGCATAAAGAGTGACCTTGGAGGGGTTTGGTGTCTTGTCAAACTGTACATACCCAGAGG 1425
QY 241 CATACAGATGACATTTGTGTTTTTAAACGGACACACGGTATATGAAAAATAATAACAATA 300
Db 1426 CTTACAGATTAGACTTTGTGTTCTTCAACGGTGCACGGCTCTATGAGAACATGGAACA 1485
QY 301 ATGATTTCTGTATACAAATAGAAAGCACCATGGATGAAAAATTTATTTGAGGATTTCTTG 360
Db 1486 ATGATTTCTGTATAGGAAATAGAAAGCACTATGAATGAAGATCTGTTTGAAGGATTTCTTG 1545
QY 361 CTGAGAAAGCAACAGAACTTGAACCTTGAACCTTGAACCTTGAACCTTGAACCTTGAAC 420
Db 1546 TTAAGAAAGCAACAGGAGCTTGAACCTTGAACCTTGAACCTTGAACCTTGAACCTTGA 1605
QY 421 AAACCTGATGAGCGCGCAATTCGAGGAAAGAAAGGCGCGCAGATAAAGCTGACAGGGTAC 480
Db 1606 AGACTGAGAAACAGCGCGCAATTCGAGGAAAGAAAGGCGCGCAGATAAAGCTGACAGG 1665
QY 481 AAGCCAAAGTTGAGTGTAGAGCAAGAAATTAATTTGCAATGATTTGAGGTTTACCCA 540
Db 1666 AAGCCAAAGTTGAGTGTAGAGCAAGAAATTAATTTGCAATGATTTGAGGTTTACCCA 1725
QY 541 GAGCTCTGTTGATTAATTTATGTTATGTTATGTTATGTTATGTTATGTTATGTTATGTT 600
Db 1726 GAAACATGTTGTTGATTAATTTATGTTATGTTATGTTATGTTATGTTATGTTATGTT 1785
QY 601 TCAGATTGTATTATAACATAAACTCAAGACCTCTAGTTTCACTAGTACTGAGATATGATGC 660
Db 1786 TCAGATTGTATTATAACATAAACTCAAGACCTCTAGTTTCACTAGTACTGAGATATGATGC 1845
QY 661 ATGCTGCTATAAACAATGAGTGTAGTGTCTCTTTTGTGTAAGAGCTTTGTCATCATC 720
Db 1846 ATGCTGCTATAAACAATGAGTGTAGTGTCTCTTTTGTGTAAGAGCTTTGTCATCATC 1905
QY 721 ATGACAAAGATTGTGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 780
Db 1906 ATGACAAAGATTGTGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1965

AC	AAD33324;
XX	(ALLE/) ALLEN S M.
DT	(BECK/) BECKLES D M.
XX	(THOR/) THORPE C J.
DE	Allen SM, Beckles DM, Thorpe CJ;
XX	Rice starch synthase DU1 homologue cDNA #1.
XX	Rice; starch synthase; DU1; enzyme; transgenic plant; genetic mapping;
KW	starch synthesis; gene; ss.
OS	Oryza sativa.
XX	Location/Qualifiers
FH	7..357
CDS	/start= a
FT	/product= "Rice starch synthase DU1 homologue protein"
FT	/note= "CDS does not include start and stop codon"
FT	/partial
US2002029394-A1.	
07-MAR-2002.	
18-DEC-2000;	2000US-00739438.
22-DEC-1999;	99US-0171514P.
(ALLE/) ALLEN S M.	
PA	(BECK/) BECKLES D M.
PA	(THOR/) THORPE C J.
XX	Allen SM, Beckles DM, Thorpe CJ;
PI	WPI: 2002-291589/33.
DR	P-PSDB; AAE20906.
XX	Novel isolated starch synthase DU1 homolog polypeptide and polynucleotide
PT	which is useful for transforming a cell and producing a transgenic plant
PT	having altered level of starch synthesis and carbohydrate composition.
XX	Claim 8; Page 14; 18pp; English.
PS	The invention relates to isolated starch synthase DU1 homologue
XX	polypeptides and their polynucleotides. The polynucleotide is useful for
CC	transforming a cell and for producing a transgenic plant by transforming
CC	a plant cell with the polynucleotide and regenerating a plant from a
CC	transformed plant. The polypeptide is useful as probes for genetically and physically
CC	mapping the gene that they are a part of, and as markers for traits
CC	linked to those genes. The polynucleotide is useful for creating
CC	transgenic plants in which the polypeptide is present at higher or lower
CC	levels than normal or in cell types or developmental stages in which they
CC	are not normally found, for altering the level of starch synthesis and
CC	carbohydrate composition in the plants, and to design and produce primers
CC	or probes. The present sequence is rice starch synthase DU1 homologue
CC	cDNA
Sequence 548 BP; 156 A; 121 C; 113 G; 155 T; 0 U; 3 Other;	
Query Match	11.2%; Score 290.6; DB 6; Length 548;
Best Local Similarity	79.9%; Pred. No. 2.9e-75;
Matches 341; Conservative	0; Mismatches 86; Indels 0; Gaps 0;
QY	1661 CAGGCGATGACCGCGATTGGCTTCTTCGTGCTCTAGATTTCTCTCA 1720
DB	3 CAGCAATGACGAGTAGAATTGGCTTCTTCGTGCTCTAGATTTCTCTCA 62
QY	1721 AAGTGGATCTTCGGAACAATATACATTTGCCATGTTGCTCAAGTGCTCTCTGTGCTG 1780
DB	63 AAATGGATCTTCCTCGATATATACATTTGCCATGTTGCTCAAGTGCTCTCTGTGCTG 122
QY	1781 GCTACAGAAGAAACTACGGAAGTCTAGCTTGGCAAACGCACGGGTGTAATACCAT 1840
DB	123 GCTATTCGAAGAACATATGCTCAAAATGGACTGTCAAAATGGGGGGTGTATTTACCAT 182
QY	1841 CCACAATCTGAATTGAGCGGATCATATTGGCAAGCAATAGATTTCTGATAAGC 1900
DB	193 CCACAACCTTGAATTGGTGACATCATATGCGCAAGCAATGCGATTTGTATAGGC 242
QY	1901 AACAACTGCTCTATACATATTCAAAGAAAGTGCAGTGCATGTCATAGTCTCTCA 1960
DB	243 TACAACCTGTTTCATATACGATTTCAAGGAAAGTGTACGACATGGTGTATTCGCCCTCA 302
QY	1961 TCTTGGAAATCTATGCGATTTCTCAATGGAATTCATCGGATATATGGATTCGTACAA 2020
DB	303 CTITTCCTANTTCCACGGTATTCGTAACGGAATTCATCCAGATATTTGGATTCATACAG 362
QY	2021 TGACAATTTATCCCGGTCCATACACTTGTAGAAATGTTGTGAAGCAAGAGGGTGC 2080
DB	363 TGACAATTTATCCCGGTCCATACACTTGTAGAAATGTTGTGAAGCAAGAGGGTGC 422
QY	2081 TAGAGG 2087
DB	423 CAAAAAG 429
RESULT 15	
AAD33324	standard; cDNA; 437 BP.
ID	AAD33324
XX	XX

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 20, 2004, 05:03:49 ; Search time 211 seconds

(without alignments)
6832.997 Million cell updates/sec

Title: US-10-634-262-1_COPY_2425_5022

Perfect score: 2598

Sequence: 1 agctgtgtaaaaaattat.....gctgaacagggcgatctcag 2598

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2598	100.0	6027	2	US-08-968-542C-1
2	2598	100.0	6027	4	US-09-554-467A-1
3	1500.4	57.8	4121	4	US-09-638-524A-1
4	1204.8	46.4	4168	3	US-08-836-567-11
5	1204.8	46.4	4168	4	US-09-606-304-11
6	931	35.8	2303	3	US-08-836-567-1
7	931	35.8	2303	4	US-09-606-304-1
8	175	6.7	212	4	US-09-313-294A-101
9	145	5.6	2652	3	US-09-115-704-1
10	145	5.6	2652	4	US-09-780-115-1
11	144.8	5.6	3434	4	US-09-388-743-9
12	111.8	4.3	2380	1	US-08-572-951-3
13	85.6	3.3	2097	3	US-08-941-445A-10
14	83.6	3.2	1248	4	US-08-489-039A-3687
15	83.6	3.2	1536	4	US-09-489-039A-3862
16	77.4	3.0	2202	4	US-09-388-743-1
17	74.4	2.9	2825	4	US-09-196-390-5
18	72.6	2.8	7218	1	US-08-232-463-14
19	69.6	2.7	1798	4	US-09-345-214-16
20	69.6	2.7	1798	4	US-09-743-980-16
21	69.6	2.7	2019	4	US-09-345-214-15
22	69.6	2.7	2019	4	US-09-743-980-15
23	69.6	2.7	2248	4	US-09-345-214-20
24	69.6	2.7	2248	4	US-09-743-980-20
25	67.2	2.6	2176	4	US-09-388-743-13
26	67	2.6	1464	1	US-07-735-085-1
27	67	2.6	1464	1	US-08-469-202-11

28	67	2.6	1464	2	US-08-484-434C-11	Sequence 11, Appli
29	67	2.6	1464	4	US-09-384-361-11	Sequence 11, Appli
30	66.8	2.6	2067	4	US-09-388-743-21	Sequence 21, Appli
31	66	2.5	2239	4	US-09-196-390-1	Sequence 1, Appli
32	65.6	2.5	2542	3	US-08-941-445A-6	Sequence 6, Appli
33	63.2	2.4	1230025	4	US-09-198-452A-1	Sequence 1, Appli
34	62.6	2.4	1650	4	US-09-252-991A-8097	Sequence 8097, Ap
35	62.6	2.4	2145	4	US-09-252-991A-8205	Sequence 8205, Ap
36	62	2.4	1818	4	US-09-731-166-3	Sequence 3, Appli
37	62	2.4	2267	4	US-08-679-645-25	Sequence 25, Appli
38	61.4	2.4	1601	3	US-08-735-491-1	Sequence 1, Appli
39	61.2	2.4	2793	3	US-08-836-567-7	Sequence 7, Appli
40	61.2	2.4	2793	4	US-09-606-304-7	Sequence 7, Appli
41	58.2	2.2	11384	4	US-08-961-527-45	Sequence 45, Appli
42	57.6	2.2	1830121	4	US-09-557-884-1	Sequence 1, Appli
43	57.6	2.2	1830121	4	US-09-843-990A-1	Sequence 1, Appli
44	57	2.2	1528	4	US-09-345-214-6	Sequence 6, Appli
45	57	2.2	1528	4	US-09-743-980-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-968-542C-1
; Sequence 1, Application US/08968542C
; Patent No. 5981728
; GENERAL INFORMATION:
; APPLICANT: Myers, et al.
; TITLE OF INVENTION: dulli Codes For A No. 5981728el Starch
; TITLE OF INVENTION: Synthese
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McGregor & Adler, LLP
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word 6.0.1 for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,542C
; FILING DATE: No. 5981728ember 12, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D., J.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D6036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 777-2321
; TELEFAX: (713) 777-6908
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6027 bp
; TYPE: nucleic acid
; STRANDEDNESS: double-stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: cdna to mRNA
; HYPOTHEetical: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: maize
; TISSUE TYPE: endosperm
; IMMEDIATE SOURCE:
; LIBRARY: maize endosperm cdna library in

parent

```

; LIBRARY: (gcl1
; CLONE: pMgf10; pMg6a; pMgt6-2M
; US-08-968-542C-1

Query Match          100.0%; Score 2598; DB 2; Length 6027;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTTGCTGAAAAAATATTTCGCTGGGAAAACAAGTTGTTTACTTATCCAGATGTTTGA 60
Db |
Qy 2425 AGCTTGCTGAAAAAATATTTCGCTGGGAAAACAAGTTGTTTACTTATCCAGATGTTTGA 2484
Db |
Qy 61 AAGCTGATTCACAAATTTGATCTCTATTTCATTCGTCGATCTATCAGCTGTGGCCAAATGAGC 120
Db |
Qy 2485 AAGCTGATTCACAAATTTGATCTCTATTTCATTCGTCGATCTATCAGCTGTGGCCAAATGAGC 2544
Db |
Qy 121 CTGATGTACTTATCAAGAGAGCAATTCATGGGTGGAGTGGAGATTTTTCATCTGAAAAAT 180
Db |
Qy 2545 CTGATGTACTTATCAAGAGAGCAATTCATGGGTGGAGTGGAGATTTTTCATCTGAAAAAT 2604
Db |
Qy 181 TGCACAGAGCGAGCTGCGAGGGAGCTGGTGGTGTGCAAACTATACATTCCTTAAAGCAGG 240
Db |
Qy 2605 TGCACAGAGCGAGCTGCGAGGGAGCTGGTGGTGTGCAAACTATACATTCCTTAAAGCAGG 2664
Db |
Qy 241 CATACAGAAATGGACTTTGTCTTTTAAACGGACACACGGTATATGAAAAATATATAACAATA 300
Db |
Qy 2665 CATACAGAAATGGACTTTGTCTTTTAAACGGACACACGGTATATGAAAAATATATAACAATA 2724
Db |
Qy 301 ATGATTTTCGTGATACAAATGAAGACACCATGATGNAATTTTATTTGAGATTTCTTGG 360
Db |
Qy 2725 ATGATTTTCGTGATACAAATGAAGACACCATGATGNAATTTTATTTGAGATTTCTTGG 2784
Db |
Qy 361 CTGAAGAAAAAGCAACGAGAACTTGAGAACCTTGCAATAGAGAGCTGAAAGAGGAGAC 420
Db |
Qy 2785 CTGAAGAAAAAGCAACGAGAACTTGAGAACCTTGCAATAGAGAGCTGAAAGAGGAGAC 2844
Db |
Qy 421 AAACCTGATAGCAGCGCGGAATGGAGGAAGAAAGGCGCGAGATAAAGCTGACAGGGTAC 480
Db |
Qy 2845 AAACCTGATAGCAGCGCGGAATGGAGGAAGAAAGGCGCGAGATAAAGCTGACAGGGTAC 2904
Db |
Qy 481 AAGCCAAAGTTGAGGTAGAGACGAAGAAGAAATAATTTGTCGAATGTTTGGGTTTAGCCA 540
Db |
Qy 2905 AAGCCAAAGTTGAGGTAGAGACGAAGAAGAAATAATTTGTCGAATGTTTGGGTTTAGCCA 2964
Db |
Qy 541 GAGCTCTGTTGATAAATTTATGTTACATGAGGCCATCACGACTGCAAGAGAGGCTACTG 600
Db |
Qy 2965 GAGCTCTGTTGATAAATTTATGTTACATGAGGCCATCACGACTGCAAGAGAGGCTACTG 3024
Db |
Qy 601 TCAGATTTGATTTATAACATAAACTCAAGACCTCTAGTTTCACAGTACTGAGATATGATGC 660
Db |
Qy 3025 TCAGATTTGATTTATAACATAAACTCAAGACCTCTAGTTTCACAGTACTGAGATATGATGC 3084
Db |
Qy 661 ATGCTGGCTATPAACAATTTGATTTGATGGACTCTCTTTTGTGAAAGCTTTGTTCAATCATC 720
Db |
Qy 3085 ATGCTGGCTATPAACAATTTGATTTGATGGACTCTCTTTTGTGAAAGCTTTGTTCAATCATC 3144
Db |
Qy 721 ATGCAAGAATTTGATTTGGTGGTTTCAGATGTTGTCGTCCTGAAGAACATATGTTAT 780
Db |
Qy 3145 ATGCAAGAATTTGATTTGGTGGTTTCAGATGTTGTCGTCCTGAAGAACATATGTTAT 3204
Db |
Qy 781 TGGACTGGGTTTTTTCGTGACGGGCCACACAGGAGTGCAAGAAATATGACAAACAATGGAG 840
Db |
Qy 3205 TGGACTGGGTTTTTTCGTGACGGGCCACACAGGAGTGCAAGAAATATGACAAACAATGGAG 3264
Db |
Qy 841 GACATGATTTTCATGCTACCTTCCAAATAACATGACTGAGGAAGAGTATTTGGATGAAG 900
Db |
Qy 3265 GACATGATTTTCATGCTACCTTCCAAATAACATGACTGAGGAAGAGTATTTGGATGAAG 3324
Db |
Qy 901 AAGAACAAAGGATCTATACAAGGCTTCAACAAGAGAGGAGGAAGGAGGAGGCTATTATTA 960
Db |
Qy 3325 AAGAACAAAGGATCTATACAAGGCTTCAACAAGAGAGGAGGAAGGAGGAGGCTATTATTA 3384
Db |
Qy 961 AAAGGAAGGCTGAGAGAAATGCAAAAAATGAAAGCTGAGATGAAGGAAAAGACTATGAGAA 1020

```

Db 4465 ACTACACTTGTGAGAAATGTGGTTGAAGGCAAGAGGGCTGCTAAGAGGGCACTGCGAGAGA 4524
QY 2101 AGTTTGGGTTACAGCAAAATCGATGTCCCGTCGTAGGAATCGTCACTGCCCTGACAGCCC 2160
Db 4525 AGTTTGGGTTACAGCAAAATCGATGTCCCGTCGTAGGAATCGTCACTGCCCTGACAGCCC 4584
QY 2161 AAAAGGGGATCCACCTGATCAAGCATGGGATTCACCGTACACTCGAAACGGAACGACAGG 2220
Db 4585 AAAAGGGGATCCACCTGATCAAGCATGGGATTCACCGTACACTCGAAACGGAACGACAGG 4644
QY 2221 TGGTTTGGTTCAGCGCGGACTCTCGAATCCAAAGCTGAATTTGTCAACCTGGCGA 2280
Db 4645 TGGTTTGGTTCAGCGCGGACTCTCGAATCCAAAGCTGAATTTGTCAACCTGGCGA 4704
QY 2281 ATACGCTCCAGCGCTAAACCATGGAAGTGGAGCTTTCCTTGACCTACGACGAGCTTC 2340
Db 4705 ATACGCTCCAGCGCTAAACCATGGAAGTGGAGCTTTCCTTGACCTACGACGAGCTTC 4764
QY 2341 TCTCGCATCTGATATACGCTCGCTCTGACTTCAATTCCTGCTCCCATCTATATTGAGCCCT 2400
Db 4765 TCTCGCATCTGATATACGCTCGCTCTGACTTCAATTCCTGCTCCCATCTATATTGAGCCCT 4824
QY 2401 CGGCTTAACCTAGCTCGTCCGATGCGGTATGGAACCATCCCGATTCGCGCAAGACTG 2460
Db 4825 CGGCTTAACCTAGCTCGTCCGATGCGGTATGGAACCATCCCGATTCGCGCAAGACTG 4884
QY 2461 GAGGCTCTTCGACACTCTCTTCGATGCGGATGGAACCATGGAAGGACGAGCCGAGATCGAG 2520
Db 4885 GAGGCTCTTCGACACTCTCTTCGATGCGGATGGAACCATGGAAGGACGAGCCGAGATCGAG 4944
QY 2521 GCCTTGAGCCCAACGGGTTTACCTTTGACGGAGCTGTATAGCAACGGTGTGACTACGGC 2580
Db 4945 GCCTTGAGCCCAACGGGTTTACCTTTGACGGAGCTGTATAGCAACGGTGTGACTACGGC 5004
QY 2581 TGAACAGGGCGATCTCAG 2598
Db 5005 TGAACAGGGCGATCTCAG 5022

RESULT 2

US-09-554-467A-1
; Sequence 1, Application US/09554467A
; Patent No. 6639125
; GENERAL INFORMATION:
; APPLICANT: Myers, Alan M.
; APPLICANT: James, Martha G.
; TITLE OF INVENTION: dullel Coding for a No. 6639125el Starch Synthase and Uses
; FILE REFERENCE: D6036PCT
; CURRENT APPLICATION NUMBER: US/09/554.467A
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: PCT/US98/24225
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/062,102
; PRIOR FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 37
; SEQ ID NO 1
; LENGTH: 6027
; TYPE: DNA
; ORGANISM: maize
; FEATURE:
; OTHER INFORMATION: cdna sequence corresponding to the gene encoding the
; OTHER INFORMATION: starch synthase enzyme DUL.
US-09-554-467A-1

Query Match 100.0%; Score 2598; DB 4; Length 6027;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTTGCTGAAAAAATATTTCGCTGGAAACAGATTGTTTACTTATCCAGATGATTGA 60
Db 2425 AGCTTGCTGAAAAAATATTTCGCTGGAAACAGATTGTTTACTTATCCAGATGATTGA 2484

QY 61 AAGCTGATTCAACAATTGATCTCTATTATTTCAATCGTGATCTATCAGCTGTGGCCAAATGAGC 120
Db 2485 AAGCTGATTCAACAATTGATCTCTATTATTTCAATCGTGATCTATCAGCTGTGGCCAAATGAGC 2544
QY 121 CTGATGTACTTATCAAAAGGAGCATTTCAATGGTGGAGTGGAGATTTTTTCACTGAAAAAT 180
Db 2545 CTGATGTACTTATCAAAAGGAGCATTTCAATGGTGGAGTGGAGATTTTTTCACTGAAAAAT 2604
QY 181 TGCACAAGAGAGAGCTGCGAGGGGACTGGTGGTCTGCAAACTATACATTTCTTAAGCAGG 240
Db 2605 TGCACAAGAGAGAGCTGCGAGGGGACTGGTGGTCTGCAAACTATACATTTCTTAAGCAGG 2664
QY 241 CATACAGATGACTTTGTTGTTTTTACGACACACCGTATATGAAAATATAACAATA 300
Db 2665 CATACAGATGACTTTGTTGTTTTTAAACGGACACACCGTATATGAAAATATAACAATA 2724
QY 301 ATGATTTTCGTATCAAAATAGAAAGCACCATTTGATGAAAATTTATTTGAGGATTTCTTGG 360
Db 2725 ATGATTTTCGTATCAAAATAGAAAGCACCATTTGATGAAAATTTATTTGAGGATTTCTTGG 2784
QY 361 CTGAAGAAAACGAAACGAGAACTTGAGAACCTTTGCAAAATGAGAAAGCTGAAAGGAGGAC 420
Db 2785 CTGAAGAAAACGAAACGAGAACTTGAGAACCTTTGCAAAATGAGAAAGCTGAAAGGAGGAC 2844
QY 421 AAACCTGATGACGCGCGGATGAGGAGAAAGGCGCGCAGATAAAGCTGACAGGGTAC 480
Db 2845 AAACCTGATGACGCGCGGATGAGGAGAAAGGCGCGCAGATAAAGCTGACAGGGTAC 2904
QY 481 AAGCAAGGTTGAGTGAGACGGAAGAAATAATTTGTCAATGTATTTGGGTTTAGCCA 540
Db 2905 AAGCAAGGTTGAGTGAGACGGAAGAAATAATTTGTCAATGTATTTGGGTTTAGCCA 2964
QY 541 GAGCTCCTGTTGATTAATTTATGTTACATTTAGGCCCATCAACGCTGGACAAAGGCTACTG 600
Db 2965 GAGCTCCTGTTGATTAATTTATGTTACATTTAGGCCCATCAACGCTGGACAAAGGCTACTG 3024
QY 601 TCAGATTGATTAATAACATAAACTCAAGACCTCTAGTTTCAGTACTGAGTATGATGTC 660
Db 3025 TCAGATTGATTAATAACATAAACTCAAGACCTCTAGTTTCAGTACTGAGTATGATGTC 3084
QY 661 ATGTGCTGCTATAACAATTGGATTTGATGACTCTCTTTTGTGAAAGGCTCTTCATCATC 720
Db 3085 ATGTGCTGCTATAACAATTGGATTTGATGACTCTCTTTTGTGAAAGGCTCTTCATCATC 3144
QY 721 ATGCAAAAGATTGATGTTGGTGGTTTGCAGATGTTTGCCTGAAAGAAATATGATGAT 780
Db 3145 ATGCAAAAGATTGATGTTGGTGGTTTGCAGATGTTTGCCTGAAAGAAATATGATGAT 3204
QY 781 TGGACTGGGTTTTTGTGACGGCCCAACAGGAGTGCAGGAATATGACAACTATGAG 840
Db 3205 TGGACTGGGTTTTTGTGACGGCCCAACAGGAGTGCAGGAATATGACAACTATGAG 3264
QY 841 GACATGATTTTCATGTACCTCTTCCAAATTAACATGACTGAGGAAGACTATTGATGGAAG 900
Db 3265 GACATGATTTTCATGTACCTCTTCCAAATTAACATGACTGAGGAAGACTATTGATGGAAG 3324
QY 901 AAGAACAAAGATCTATACAGGCTTCAACAGAGAGGGAAAGGAGAGAGGCTATTATTA 960
Db 3325 AAGAACAAAGATCTATACAGGCTTCAACAGAGAGGGAAAGGAGAGAGGCTATTATTA 3384
QY 961 AAAGGAGGCTGAGAGAAATGCAAAATGAAAGCTGAGATGAAAGGAAAGAACTATGAGAA 1020
Db 3385 AAAGGAGGCTGAGAGAAATGCAAAATGAAAGCTGAGATGAAAGGAAAGAACTATGAGAA 3444
QY 1021 TGTTCCTGGTTTCTCAGAAAACATTTGTTTACACCGAAACCATTTGAAATACATGCTGAA 1080
Db 3445 TGTTCCTGGTTTCTCAGAAAACATTTGTTTACACCGAAACCATTTGAAATACATGCTGAA 3504
QY 1081 CTACTATTGATGCTTTTATATTCCTTTAAACAGTTCTTAACAGTTCTTAACAGGAGGTTT 1140
Db 3505 CTACTATTGATGCTTTTATATTCCTTTAAACAGTTCTTAACAGGAGGTTT 3564
QY 1141 GGTTCGATGTTCTCTTTAATCGTTGGATGATCCAGGTGGGGTGTGCCACCTCAGAGA 1200

Db 1538 CATACAGACTAGACTTTGTATTTCTTAAACGGTGACACTGTCTATGAAATAACAATCACA 1597
Qy 301 ATGATTTTCGTGATACAAATAGAAAGCACCATGATGAAATTTATTTGAGATTTCTTGG 360
Db 1598 ACGATTTTTTCTCGAATAGAAAGTGCATGATGAACTCATTTTGGAGACTTCTTGG 1657
Qy 361 CTGAAGAAAAGCAACGAGAACTTGAGAACCTTGCMAATGAGGAGCTGAAAGAGGAGAC 420
Db 1658 TTGAAGAAAAGCGAAGAACTCGAGAGCTTGTGCGAGAAGAGCTGAAGGAAAGAC 1717
Qy 421 AAACGTGATGACGCGCGGATGAGGAGAAAGGCGCGAGATAAAGCTGACAGGGTAC 480
Db 1718 AAGCTGAGGAGCGGCA CAGGAGAGAGAAAGGCGCGGATGGAAGCTGACAGGGCAC 1777
Qy 481 AAGCCAGGTTGAGTAGACGAGAAAGAAATTAATTTGTCNAATGTTGGTTTACCCA 540
Db 1778 AAGCAAGCTCTGAGGTGAGATGAGAAAGAAAGAAATTTGCGCCAGATGTTGAGTTCCGCTA 1837
Qy 541 GAGCTCCTGTTGATTAATTTATGTTACATTTAGGCCCATCAGACTGGCAAGAGGCTACTG 600
Db 1838 GCAGATATGCTGAGAACTTATGTTGATACATAGAACTTAACACTACAGAGGAGACAGAG 1897
Qy 601 TCAGATTTGATTAATACATTAACCTCAAGACCTCTAGTTTCCAGTACTGAGATATGAGATGC 660
Db 1898 TTAGATTTGATTAATAGAGCTCGAGATCACTAATGCAATAACACTGAGATTTGGATGC 1957
Qy 661 ATGTTGCTTATAACAAATTTGATGATGACTCTCTTTTGTGAAAGGCTTGTTCATCATC 720
Db 1958 ATGAGGTTTATAACACTGATGATGACTCTCAATAGCTGAAAGACTTGTCAATCTC 2017
Qy 721 ATGACAAAGATTTGATTTGTTTTCAGATGTTTGTGCTGCTGAAAGAAACATATGAT 780
Db 2018 ATGAAAAGGAGCGAATTTGTTGTTATCTAGAACTTACATTTACCTGAAAGGCAATTTGTTGT 2077
Qy 781 TGAAGTGGTTTTTGTGACGGCCACAGGAGTGCAGGAATTAATGACAAATGGAG 840
Db 2078 TGATTTGGTTTTTGTGATGAGCACTCGGATGCAAGGAATTAATGATAACAAATGGAA 2137
Qy 841 GACATGATTTTCATGCTACCTTCCAATTAACATGACTGAGGAGAGATTTGATGGAAG 900
Db 2138 GGCAGGATTTTCATGCCATCTGTTCTTAATTAACATATCGATGATATCTTTTGGTGGAG 2197
Qy 901 AAGAACAAAGGATCTATACAGGCTTCAACAAAGAGGAGGAGGAGGAGGCTATTA 960
Db 2198 AAGAACATAGGATCTTTACAGGCTTCAACAGAGAGAGAGAAAGGAGGAGTSCOGAAA 2257
Qy 961 AAGGAGGCTGAGAGAAATGCAAAAATGAAGCTGAGATGAAGGAAAGAACTATGAGAA 1020
Db 2258 GAATAAAGGCTGAGAGATCTGCAAAAATGAAGCTGAGATGAAGGAAAGAACTATGAGAG 2317
Qy 1021 TGTTCCTGTTTCTCAGAAAACATTTCTTACCCGAAACCACTTGAATATACATGCTCGAA 1080
Db 2318 CGTTCTGCTCTACAAAACATATTTGTATATCTAGAGCACTCGAAGTACGTGAGAGAA 2377
Qy 1081 CTACTATGATGCTTTTATAACCTTCTAATACAGTTCTAATCTGAAAGCCAGAGTTT 1140
Db 2378 CCACTGTGAGCGTTCTTTATAATCTTTCTAACACAGTCTGAATGGAAGAGTCAAGAGTTT 2437
Qy 1141 GGTTCATGTTCTTTAATCGTTGGATGATCCAGGTGGGTGTTGCCACCTCAGAA 1200
Db 2438 GGTTCAGAGGTTCTTTAAACCGTTTGAACATCCAGTGTGCCCTTACCCACCAAGAA 2497
Qy 1201 TGGTACAGCAGAAAATGGTTTCAACCTTAAAGCAACAGTTTACGTTTCCACGAGATCCCT 1260
Db 2498 TGGTAAAGGCTGAGAAATAGTTTCACTTACGAACACAGCTCAGTTTCCCTGGATGCAT 2557
Qy 1261 ATATGATGGAATTTGTTTTCTCGAGTGCAGAAAGGTGGAATTTATGATAACAGAAATG 1320
Db 2558 ATATGATGGAATTTGTTTTCTCTGAGTCGGAAGAGGTGGAAGATATGACAAATAGGAACG 2617
Qy 1321 GGTTAGACTATCATATTTCTGTTTTTGGTTCATTTGCAATGCAAGGAAACCACTATGCAATTTG 1380
Db 2618 GGAATGGAATTCATATTTCTGTGTCTGATTCGGTTGCAAGGGAACCTCCCAATGCAATTTG 2677

Qy 1381 TCCACATTCCTGTTGAGATGCGACCAATCGCAAGGTTGAGGCTTTGGTGATGTTCTCA 1440
Db 2678 TACACATTCAGTGGAAATGGCTCTTATCGCAAGGTTGGAGCCCTTGGTGATGTTGTTA 2737
Qy 1441 CTAGTCTTTTCCACGTGCTGTGCAAGATTTAGGACACAAATGTGGAGGTTATTTCTCCAAAGT 1500
Db 2738 CAAGCCCTTTCCACGAGCTGTTTCAGGAATTTAGGCCATTAAGTTGAGGTTATTTCTGCCGAAGT 2797
Qy 1501 ACGTTTCTTGAATCTAAGCAATGTCAAGATCTCAAAATCCATCAAGTCTTTCTTGGG 1560
Db 2798 ATGATTTGTTTAAATCCCTAAGCAGTGTGAAGATTTACATACCAACAAAGTTTGTCTCGG 2857
Qy 1561 GTGGTTCTGAAATAAATGTGGCGTGGACTAGTCGAAGGCTTTGTGTTTATCTTCTG 1620
Db 2858 GTGGCACAGAGGTAAAGTATGTTTGGAAAGGTTGAAGATCTGCCAGTTTATCTTCTTGG 2917
Qy 1621 AACCTCAAAATGGATGTTTGGAGTCGGATATCTATATGCGAGGACGATGACCGCCGAT 1680
Db 2918 AACCAAAAATGSCATGTTTGGGTTGGATGTGTATGGGAAGATGATGAGAGTAGAT 2977
Qy 1681 TTGGCTTCTTCTGTCGTTCTGCTCTAGAGTTTCTCTCMAAGTGGATCTTTCCGAAACA 1740
Db 2978 TTGGCTTCTTCTGTCATTTCTGCTCTGAGTTTCTGCTCCAAAAGGATCTTCTCTGATA 3037
Qy 1741 TAATACTTGCATGATTTGTCGAAGTCTCTCTGCTGGCTACACAAGAAACTACG 1800
Db 3038 TCAATATTTGCTGACTGCTCAAGTCTCCCGTTGCTTGGCTATACAAGAAACAGTATG 3097
Qy 1801 CGAAGCTTAGCTTTGGCAACGCGCGGTGTTTACCATCCACAACTTTGAATTTGAG 1860
Db 3098 CTCCTTAATGGCTGGGAAATGGTCCGATTCTATTTACCATCCCAATCTTTGAGTTGAG 3157
Qy 1861 CGCATCATATTTGGCAAGCAATGAGATATTTGTAATGAAGCAACAATGCTCTTAATACAT 1920
Db 3158 CGCATCACATTTGGCAAGGCAATGGCACTTTGTGCAAGGCTACAACTGTCTCTGATACAT 3217
Qy 1921 ATTCAAGGAGGTTGTCAGGTCATGGTGCCATAGTTCTCTCATCTTTGGGAAATTTCTATGGCA 1980
Db 3218 ATTTCAAGGAGGTTGGCTGGACATGGAGCTATTTGCACTCACTATAAATTTCCATGGAA 3277
Qy 1981 TTCTCAATGGAATTTGATCCGGATATATGGGATCCGTACAAATGACAACTTTATCCCGTCC 2040
Db 3278 TTGCAATGGAATTTGATCCCTGACATTTGGGATCCATATACTGACAGATTTATTTCCCGTTC 3337
Qy 2041 ACTACACTTTGTGAGATTTGTTGAGGCAAGGCTGCTAAGAGGGCTATGAGGGCTATGAGGAGA 2100
Db 3338 ATTATACATCAGAGAATGTTCTTTGAGGGCAAGGCTGCTGCAAAAAGGSCATTTGAGCAGA 3397
Qy 2101 AGTTTGGGTTTACAGCAAAATCGATGTCCCGTCTGAGGAATCGTCACTCGCTGACAGCCC 2160
Db 3398 TGCTTGGATTTACAGCAAACTGATAGCCCTGTTTGTGAATCATCTCTGTTCTAACAGTGC 3457
Qy 2161 AAAAGGGAATCCACCTGATCAAGCATTCGGATTCACCGTACACTCGAAACGGAACGGAAGG 2220
Db 3458 AGAAGGGAATCCACCTTATCAAAATGCAATGCAATCGAGCTCTTGAAGCAATGGGCAAG 3517
Qy 2221 TGGTTTTGCTTGGTTTTCAGCGCCGAGCTCTCGAATCCAGCTGATTTTGTCAACCTGGCGA 2280
Db 3518 TGGTTTTTACTGGGTTCTGCACCCAGATCATGCGCATACAAGGTGACTTTTACAAATTTAGCCA 3577
Qy 2281 ATACGCTCCACGGCTTAAACCATGGGCAAGTAGGGCTTTCTTTGACTACGACGAGGCTC 2340
Db 3578 GTAACTGCTGATGATTAACCATGGCGGGTGAAGCTATGTTTAACTATGACGAGCCAC 3637
Qy 2341 TCTCGCATCTGATATACGCTTGGCTCTGACTTCAATTTCTGTTCCCATCTATATTTGAGCCTT 2400
Db 3638 TGTCACATTT----- 3647
Qy 2401 GCGGCTTAACCTAGCTCGTCCCATCGGATATGGAACCAATCCCGATTTGTCGCAAGACTG 2460
Db 3648 -----GCTTATTTGCTATGCGGTACGSAATCCATCCCGGATTTGTCGGAATACTG 3694

Db 2196 ATTTTACTGTCTCAGAAAGCATGTATATATCTAGACCTCTTGTATATCAAGCTGAAG 2255
QY 1082 TACTATTGATGTCTTTATATCTTCTATATACAGTTCTTAACCTGGAAGCCAGAGTTTG 1141
Db 2256 CAGGTACAGTTTACTATATCCCGCAATACAGTACTTAATAGGTAAACCTGAAATTTG 2315
QY 1142 GTTTCGATGTCTCTTAAATCGTTGGATGTATCCAGGTGGGGTGTGGCCACTCAGAAGAT 1201
Db 2316 GTTCAGATGTTCAATTAATCGCTGGACTACCGCTGGGTCCATTTGCCACTCAGAAAT 2375
QY 1202 GGTACAAAGCAAAATGGTTCAACCTTAAGCAACAGTTTACGTTCCACGAGATGCCA 1361
Db 2376 GTCCCTGTCTGAAATGGCAACCATGTCCAGAACTGTGAAGTTCATTTGGATGCATA 2435
QY 1262 TATGATGCACTCTGTTTCTCGAGTCAGAGAGGTGGAAATTTATGATAACAGAAATGG 1321
Db 2436 TATGATGGAATTTGTATTTCCGAGAGAGAGATGGTGGGATTTTTCACAAATAGAGCGG 2495
QY 1322 GTTAGACTATCATATCTCTGTTTGGGTCAAATTTGCAAGGAACCACTATGCACATTTG 1381
Db 2496 AATGGACTATCATATCTCTGTTTGGAGGAGTGCCTAAAGAACCTCCAATGCATATTTG 2555
QY 1382 CCACATGCTGTTGAGATGCAACATTCGAAGGTGGAGGCTTGGTGAATGTTGCAC 1441
Db 2556 CCATATTTGCTGTGAAATGSCCAATTTGCAAGGTGGAGGCTTGGTGAATGTTGTAC 2615
QY 1442 TAGTCTTTACGTGCTGTGCAAGATTTAGGACACAATGTGGAGTATTTCTTCCAAAGTA 1501
Db 2616 TAGTCTTTCCGTGCTGTTCAAGATTTAAACCAATATGTGATATATCTTACCTAAGTA 2675
QY 1502 CGGTGCTTGAATCTAAGCAATGTCAAGATTTCAAAATCCATCAGAGTTTTTCTTGGGG 1561
Db 2676 TGACTGTTTGAAGATGAATAATGTGAAGGACTTTCGGTTTCAAAAACACTTTTGGGG 2735
QY 1562 TGGTCTGAAATAAATGTGTGGGTGAGTGTAGTGAAGGCTTGTGTTTACTTCTGGA 1621
Db 2736 TGGGACTGAATAAAGATGATGGTTGGAAGGTGGAGGTCTCTCGCTCTATTTTGGGA 2795
QY 1622 ACCTCAAAATGGGATGTTTGGAGTCGGATATGTATATG---GCAGGACCATGACCGCG 1678
Db 2796 GCTCAAAACGGGTATTTTTCGAAGGGTGGCTATGGTTGTAGCATATGATGGTGAACG 2855
QY 1679 ATTTGGCTCTCTGTCGTCTGCTCTAGAGTTTCTCTCAAAAGTGGATCTTCTCGAA 1738
Db 2856 ATTTGGTTTCTCTGTCAACGGCTTTTGGAGTTTCTCTCAAGGTGGAATTTAGTCGGA 2915
QY 1739 CATATACATTCGATGATGGTCAAGTCTCTGTTGCTTGGCTGCTACAGAAACTA 1798
Db 2916 TATCATTCATTCGATGATGGTCTAGTCTCTGTTGCTTGGCTCTTTAAGGAACAATA 2975
QY 1799 CGCGAAGTCTAGCTTGGCAACGACGGGTGGTATTCACCATCCAAATCTTGAATTTGG 1858
Db 2976 TACACACTATGTTCTAAGCAAACTCGTATAGTCTTCAGATACATATCTTGAATTTGG 3035
QY 1859 AGGCTATATTTGGCAAGCAATGATATGTGATAAGCAACACTCTCTCTAATAC 1918
Db 3036 GGCAGATCTCATTTGGGAGCAATGACTAACGCGACAAAGTCAACAGATTTTCAACCAAC 3095
QY 1919 ATATTCAAAGGAGTGTCAAGTCAATGTCATGTTCTCTCTTGGGAAATCTATGG 1978
Db 3096 TTTACTCAGAGGAGTGTCTGGAACCTGTPAATTTGGCCCTCACCTTCAAGTTCCATGG 3155
QY 1979 CATTTCAATGGAATTTGATCCGGATATATGGGATCCGTACAAATGACAACTTTATCCGGT 2038
Db 3156 TATAGTGAATGGATGACCCAGATATTTGGGATCTTTTAAAGATAAGTTCAATTCGAT 3215
QY 2039 CCACATCATTTGTGAGATGTTGTGAAGCAAGAGGGCTGTGAAGGGCACTGACGA 2098
Db 3216 TCCGTACACCTCAGAAAACCTTGTGAAGGCAAAAACAGACCAAGCAAGCACTTTGACGCG 3275
QY 2099 GAATTTGGTTACAGCAATTCATGTCCTCCGCTGCTAGGAATGTCCTGCTGCTGACG 2158
Db 3276 AAAAATGGACTGAAACAGGCTGACCTCTCTTGGTAGGAATTTATCACCGCTTAACTCA 3335

QY 2159 CCAAAAGGGATCCACTGTATCAAGCATCGATTACCGTACACTCGAAACGACGACA 2218
Db 3336 CCAGAAAGGAATCCACTCAATTAACATGCTATTTGGCGCACCTTGGAAACGGAAC 3395
QY 2219 GGTGGTTTTTCTTGGTTTCAGCGCGGACTCTCGAATCCAACTGATTTTGTCAACCTGGC 2278
Db 3396 GGTAGTCTTGGTTTCTGCTCTGATCTAGGGTACAAACGATTTTCTTAATTTGGC 3455
QY 2279 GAATAGCTCCACGGGTAAACCATGGGCAAGTGAAGCTTTTCCCTGACCTACGACGACC 2338
Db 3456 AAATCAATTTGCACTCAAAATATATGACCGCGCACGACTCTGTCTAATATGACGAGCC 3515
QY 2339 TCTCTCGACTCTGATATAGCTGCTGACTTCAATCTGTTGCCATCTATATTTGAGCC 2398
Db 3516 ACTTCTCACCTGATATATGCTGCTGATTTTATTTCTAGTTCTTCAATATTTGAGCC 3575
QY 2399 TTCCGGCTTAACCTCAGCTCTGCCATGCGGTATGGAACCATCCGATTTCTCCGCAAGAC 2458
Db 3576 ATCTGGACTAAACAACACTTACCGCTATGAGATATGTTCAATTCAGTCTGCGTAAAC 3635
QY 2459 TGAAGGCTCTTCGACACTGTCTTCGATGTGGACAATGACAAGAACGACCCGAGATCG 2518
Db 3636 TGAAGGACTTTATGATACTGTATTTGATGTGACCATGACAAAAGAGAGACAAACAGT 3695
QY 2519 AGCCCTTGAGCCCAACGGGTTTAGCTTTGACGAGCTGATAGCAACGGTCTTGACTACGC 2578
Db 3696 TGTCTTGAACCAATGGATTCAGCTTTGATGGAGCATGCTGGCGGAGTTGATATGC 3755
QY 2579 GCTGAACAGGGCATCTCAG 2598
Db 3756 TCTGAATAGACTCTCTCTG 3775

RESULT 5

US-09-606-304-11
; Sequence 11, Application US/09606304
; Patent No. 6483010
; GENERAL INFORMATION:
; APPLICANT: Kossmann, Jens
; Springer, Franziska
; Abel, Gernot
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
; PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/606,304
; FILING DATE: 28-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,567
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE P 44 41 408.0
; FILING DATE: 10-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Agrevo-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000

TELEFAX: 212-586-9090
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4168 base pairs
TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to RNA
ORIGINAL SOURCE:
ORGANISM: Solanum tuberosum
STRAIN: cv. D, sir, e
TISSUE TYPE: leaf tissue
IMMEDIATE SOURCE:
LIBRARY: cDNA-library in Lambda ZAPII
OTHER INFORMATION: CDS
FEATURE:
LOCATION: 307...3897
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-606-304-11

Query Match 46.4%; Score 1204.8; DB 4; Length 4168;
Best Local Similarity 66.7%; Pred. No. 0;
Matches 1735; Conservative 0; Mismatches 862; Indels 3; Gaps 1;

QY 2 GCTTCTGAAAAAATTATTCCTCGGGAACAAAGTTGTTTACTTATCCAGATGTATTGAA 61
Db |||||
QY 62 AGCTGATTCACAAATGATCTCTATTCAATCGTGTATCATCGTGTGCGCAATGAGCC 121
Db |||||
QY 1236 ACCTGATGAAGATGTCGAGATATTCTTAAACAGAGGTCCTTCCACTTTGAAGAAATGATC 1295
QY |||||
QY 122 TGATGTACTATPAAAGAGGACATCAATGGGTGGAAAGTGGAGATTTTCACTGAAAAATT 181
Db |||||
QY 1296 TGATGCTTGATTATGGAGCTTTTAAAGAGTGGCGCTATAGTCTTTTACTAAGGCT 1355
QY |||||
QY 182 GCACAAAGAGCGCTGGCAGGGAATGTTGGTGTGCAAACTATACATTCCTTAAGCAGGC 241
Db |||||
QY 1356 AACTGAGACTCATCTCAATGGAGATGTTGGTCTTGAAGATCCATGTTCCCAAGGAAGC 1415
QY |||||
QY 242 ATACAGATGACATTTGTTGTTTAAACGGACACACAGGTATAGAAATATAACAAATAA 301
Db |||||
QY 1416 ATACAGGCTGATTTTGTGTTTTTAAATGGACAGATGCTATGACAAATGATGGA 1475
QY |||||
QY 302 TGATTCGTGATACAAATAGAAAGCACCATGGATGAAAATTTATTTGAGGATTTCTTGGC 361
Db |||||
QY 1476 TGACTTCAGTATACTGTGAAAGGTGGTATGCAATCATTTGACITTTGAAATTTCTTGT 1535
QY |||||
QY 362 TGAAGAAAGCAACGAGAACTTGAAACCTTGCAATAGGAGAGCTGAAAGAGGAGACA 421
Db |||||
QY 1536 TGAGAGAAATGGAGAGAACAGGAGAACTTGTAAAGAAACAAAGCTGAAAGAGAAAGACT 1595
QY |||||
QY 422 AACTGATGAGCAGCGGGAATGGAGAGAAAGGCGCAGATRAAGCTGACAGGTACA 481
Db |||||
QY 1596 AGCGGAAGAACAAAGACCAATAGACAGAGAAAGCTGAATTTGAAGCTGACAGACACA 1655
QY |||||
QY 482 AGCCAAGGTTGAGTGAAGACGAGAGAAATTAATTTGTGCAATGATTTGGTTTGGCCAG 541
Db |||||
QY 1656 AGCAAGGAAGAGGCTGCAAGAAAAGAAAGTATTTGCGAGAAATTTGATGTTAAAGCCAC 1715
QY |||||
QY 542 AGCTCCTGTTGATTAATTTATGATGATTTGAGCCCATCAGCTGCAAGAGGCTACTGT 601
Db |||||
QY 1716 GAAGACTCGTATATCAAGTGGTATAGAGCAAGTGAATTTAAATCCGAGGACAAGGT 1775
QY |||||
QY 602 CAGATTGTATTATAACATAAAGCTCAAGACCTCTAGTTTCAAGATCTGAGATATGATGCA 661
Db |||||
QY 1776 CAGTTTACTATAACAAAGTTTCAAGTCTCTCTCCATGCTAAGGACTTGTGATCCA 1835
QY |||||
QY 662 TGGTGGCTATAACAAATGAGTGAAGTCTCTCTTTTGTGCAAGGCTTGTTCATCAATCA 721
Db |||||
QY 1836 CGGAGGATATAATTTGGAAGGATGTTTGTCTATTGTCAAAAGCTTTTAAATCTGA 1895
QY |||||
QY 722 TGACAAAGATTTGATGGTGGTGGAGATGTTGCTGCTGCTGAAAGAACATATGTTATT 781
QY |||||

Db |||||
QY 1896 GAGATAGATGGTATGGTGTATACAGAGTTGTTTATTCCTGATCAGGACATTTCTT 1955
QY |||||
QY 782 GGACTGGGTTTTGCTGACGGCCCAACAGGAGTGCAGGAATATGACAAATGAGG 841
Db |||||
QY 1956 GGATTGGGTTTTGCTGATGGTCCACCACCAAGCATGCCATTGCTTATGATAACAATCACCG 2015
QY |||||
QY 842 ACATGATTTTCATGCTACCCCTTCGAAATPAAACATGACTGAGGAGAGTATGATGAAGA 901
Db |||||
QY 2016 CCAAGACTTCCATGCCATTGTCGCCCAACCACTCCGAGGAATTTATTTGGGTTGAGA 2075
QY |||||
QY 902 AGACAAAGGATCTATACAAGCTTCAACAAGAGAGGAGGAAAGGAGGAGCTATTAA 961
Db |||||
QY 2076 AGAATCATCAGATCTTTAAGACACTTCAGGAGAGAGAGGCTTAGAGAGGGCTATGCG 2135
QY |||||
QY 962 AAGNAGGCTGAGAGAAATGCAAAATGAAAGCTGAGATGAAGGAAAAAGACTATGAGAA 1021
Db |||||
QY 2136 TGCTAAGGTTGAAAAAAGCAGCACTTCTGAAACCTGAAACAAAGGAAAGAACTATGAAATC 2195
QY |||||
QY 1022 GTTCTGGTTCCTCAGAAACACATTTTACACCGAACCACTTGAATACATCTGGGAC 1081
Db |||||
QY 2196 ATTTTACTGCTCAGAAAGCATGTAGTATATACAGCTCTTGTATATCCAGCTGGAAG 2255
QY |||||
QY 1082 TACTATTGATGCTCTTATAATCTTCTAATACAGTCTTAACTGGAAGCCAGAGTTTG 1141
Db |||||
QY 2256 CAGCTCACAGTTTACTATATATCCGCCAATACAGTACTTAAATGGTAAACCTGAAATTTG 2315
QY |||||
QY 1142 GTTTCGATGTTCTTTAAATCGTTGGATGTATCCAGGTGGGTGTTGCCACTCAGAAAT 1201
Db |||||
QY 2316 GTTCAGATGTTTCAATTAATCGTGCATCCCGCTGGGTCCATTTGCCACCTCAGAAAT 2375
QY |||||
QY 1202 GGTCAAGCAGAAATGTTTCAACCTTAAAGCAACAGTTTTACGTTCCACAGATGCCCTA 1261
Db |||||
QY 2376 GTGCGCTGCTGAAATGSCACCATGTGAGAGCAACTGTGAAGTTCATTTGGATGCATA 2435
QY |||||
QY 1262 TATGATGACTTCGTTTTCTCGAGTGCAGAAAGGTGGAATTTATGATAACAGAAATG 1321
Db |||||
QY 2436 TATGATGATTTTGTATTTTCCGAGAGAGAAAGTGGTGGATTTTGAACAATAAGAGCG 2495
QY |||||
QY 1322 GTTAGACTATCATATTCCTGTTTTTGGGTCAATTTGCAAGGAACCACTATGCAATGT 1381
Db |||||
QY 2496 AATGACTATCACATACCTGTGTTTGGAGGAGTCCCTAAAGAACCTCCAATGCTATTGT 2555
QY |||||
QY 1382 CCACATGCTGCTGAGATGGCAACATCGCAAGTGTGAGGTCTTGGTGTATGTTGCAC 1441
Db |||||
QY 2556 CCATATTGCTGTGCAATGGCAACCAATGCAAGGTGGAGGCTTGGTGTATGTTGTAC 2615
QY |||||
QY 1442 TAGTCTTTACGTGCTGCAAGATTTAGGACACAATGTGGAGGTATTTCTTCCAAAGTA 1501
Db |||||
QY 2616 TAGTCTTTCCGTCGTCTCAAGATTTAAACCAATAATGTGGATATTATCTTACCTAAGTA 2675
QY |||||
QY 1502 CGGTGCTTGAATCTAAGCAATGTCAAGATCTCAAAATCCATCAGATGTTTTCTTGGGG 1561
Db |||||
QY 2676 TGACTGTTGAAGATGAATATGTGAAGGACTTTTCGGTTTCAAAAAAATCTACTTTTGGGG 2735
QY |||||
QY 1562 TGGTTCTGAAATAAATGTGGCGTGGACTAGTCCAAAGGCTTTGTGTTTACTTCTCGGA 1621
Db |||||
QY 2736 TGGGACTGAAATAAAGATGTTTGAAGAGTGAAGGCTCTCGTCTATTTTGGGA 2795
QY |||||
QY 1622 ACCTCAAAATGGGATGTTTGGAGTCCGATATGTAATG---GCAGGAACGATGACCGCG 1678
Db |||||
QY 2796 GCCTCAAAACGGGTTATTTTCGAAAGGCTGCTATGTTGTGAACATGATGTTGAAACG 2855
QY |||||
QY 1679 ATTTGGCTTCTTCGTCTCTCTAGAGTCTTCTCTCCAAAGTGAATCTTCTCCGAA 1738
Db |||||
QY 2856 ATTTGGTCTTCTTCGTCCCGGCTTTGGAGTTTCTTCTGCAAGGTGGAATTTAGTCCGGA 2915
QY |||||
QY 1739 CATATAATTTGCAATGATTTGGTCAAGTCTCTCTGTTGCTGCTGCTACACAGGAAAACTA 1798
Db |||||
QY 2916 TATCATTTGATGCAATGATTTGGTCTAGTCTCTCTGTTGCTTGGCTCTTTAAGGAACTA 2975
QY |||||
QY 1799 CGCAAGCTTAGCTGTCGCAACGCAAGGTTGGTATTCACCATCCCAATCTTGAATTTGG 1858
QY |||||

Db 2976 TACACACTATGCTCTAAGCAATCTCGTAGTCTTTCACGATACATAATCTTGAATTTGG 3035
QY 1859 AGCGCATCATATTTGGCAAGCAATGAGATATTGTGATAAGCAACAACCTGTCTCTAATAC 1918
Db 3036 GCGCATCTCATTTGGGAGAGCAATGATACACGAGCAAAAGCTTACAACTTTTCCAAAC 3095
QY 1919 ATATTCAAAGGAAGTCTCAGGTCAATGGTCCATAGTTCCTCATTTTGGGAAATTCATGG 1978
Db 3096 TTACTCAGAGGAGTGTCTGGAACCCCTGTAATTTGGCTTCCCTTCAAGTTCATGG 3155
QY 1979 CATTCTCAATGGAATGATCCGGATATATGGATCCGTACAAATGACAACCTTTATCCCGGT 2038
Db 3156 TATAGTGAATGGATTTGACCCAGATATTTGGGATCCTTTAAACGATAAGTTCATTCGGAT 3215
QY 2039 CCACATACACTTGTGAAATGTTGTTGAAGGCAAGAGGCTGCTTAAGAGGCACTGAGCA 2098
Db 3216 TCCGTACACCTCAGAAAAGCTTTGAAGGCAAAAAGAGGCAAGAGGCTTTGAGCG 3275
QY 2099 GAAGTTTGGGTTACAGCAATCGATGTCCCGGTCTGAGGAATCGTCACTCGCTGACAGC 2158
Db 3276 AAACTTGGACTGAACAGGCTGACCTTCTTTGGTAGGAATATCACCGCTTAATCTCA 3335
QY 2159 CCAAAAGGGATCCACTGATCAGCATGAGATGATCCGTTACCTGACAGCGGAACGGACA 2218
Db 3336 CCAGAAAGGAATCCACTCATTTAAACATGCTATTTGGCGCACCTTGGAAACGGAAACGACA 3395
QY 2219 GGTGTTTGTGTTGTTGACGCGGACCTCTGAAATCCAGCTGATTTTGTCAACCTGGC 2278
Db 3396 GGTAGTCTTGTGTTGTTGCTCTGATCTAGGTTACAAAAGATTTTGTAAATTTGGC 3455
QY 2279 GAATACGCTCCAGCGGTAAACCATGGCAAGTGAAGCTTTCTTGACCTACGACGAGCC 2338
Db 3456 AAATCAATTTGCACCTCAATATAATGACCGGACAGACTCTGTCTAAATATGACAGCC 3515
QY 2339 TCTCTCGCATCTGATACGTGGCTCTGACTTCACTTGTGTCCTCAATCTAATTTGAGCC 2398
Db 3516 ACTTTCTCACTGATATGCTGCTGCTGATTTATTTAGTTCCTTCAATATTTGAGCC 3575
QY 2399 TTGGGCGCTAACTCAGCTCGTCCCATGGGTGGAACCAATCCCATTTGTCGCGAAGAC 2458
Db 3576 ATGTGACTTAACAACTTACCGCTATGATGATGTTTCAATTTCCAGTCTGCTGTTAAAC 3635
QY 2459 TGGAGGCTCTTCGACACTGTCTTCGATGTGGAACAATGACAAAGGACGAGCCGAGATCG 2518
Db 3636 TGGAGGACTTTATGATCTGTTATTTGATGTTGACCATGACAAAGAGAGAGCAACAGTG 3695
QY 2519 AGSCCTTGAGCCCAACGGGTTTAGCTTTGACGAGCTGATAGCAACGGTGTGACTACGC 2578
Db 3696 TGGTCTTGAACCAATGGAATTCAGCTTTGATGAGCAGATGCTGGCGGAGTTGATTATGC 3755
QY 2579 GCTGAACAGGCGATCTCAG 2598
Db 3756 TCTGAATAGCTCTCTCTG 3775

RESULT 6
US-08-836-567-1
; Sequence 1, Application US/08836567
; Patent No. 6130367
; GENERAL INFORMATION:
; APPLICANT: Kossmann, Jens
; APPLICANT: Springer, Franziska
; APPLICANT: Abel, Gernot
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
; TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA

; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,567
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04415
; FILING DATE: 09-NOV-1995
; PRIOR APPLICATION DATA: DE P 44 41 408.0
; FILING DATE: 10-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Agrevo-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2303 base pairs
; TYPE: nucleotide
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Solanum tuberosum
; STRAIN: cv Berolina
; TISSUE TYPE: tuber tissue
; IMMEDIATE SOURCE:
; LIBRARY: cDNA-library in pBluescriptSKII+
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..2033
; OTHER INFORMATION: /function= "Polymerization of starch"
; OTHER INFORMATION: /product= "Starch synthase"
US-08-836-567-1
Query Match 35.8%; Score 931; DB 3; Length 2303;
Best Local Similarity 68.5%; Pred. No. 2.2e-284;
Matches 1301; Conservative 0; Mismatches 595; Indels 3; Gaps 1;
QY 703 AAAGGCTTCTTCATCATCATGACAAAGATTGTGATTGGTGGTTTCAGATGTTGCTGTCG 762
Db 13 AAAGCTTGTAAATCTGAGAGAAATAGTGGTGGTGGTATACAGAGTTGTTATTTC 72
QY 763 CTGAAAGAACATATGATGATTGGACTGGGTTTTTCTGACGCGCCACCCAGGAGTGCAGGA 822
Db 73 CTGATCAGGCACCTTTCTTTGGATTGGGTTTTTGTGATGTCCACCCAGCATGCCATTG 132
QY 823 ATTATGACAAATGAGGACATGATTTTCATGCTACCTTCCAAATAACATGACTGAGG 882
Db 133 CTTATGATAACAATCACCGCAAGACTTCCATGCCATTGTCCCAACCAATTCGCGAGG 192
QY 883 AAGAGTATTGGATGGAAGAAGAACAAAGCATCTATACAGGCTTCAACAAGAGAGAGGG 942
Db 193 AATTATTTGGTTGAGGAAGAACATCAGATCTTTAAGACATTCAGGAGGAGAGAGGC 252
QY 943 AAAGGAGGAGGCTATTAAAGAGAGGCTGAGAGAAATGCAAAAATGAAAGCTGAGATCA 1002
Db 253 TTAGAGAAGCGCTATGCGTCTAAGGTTGAAAAAACACGCACTTCTGAAACTGAAACAA 312
QY 1003 AGGAAAGACTATGAGATGTTTCTCAGAAACACATTTGTTTACCGGAAACAC 1062
Db 313 AGGAAAGAACTATGAAATCATTTTACTCTCTCAGAAAGCATGTAGTATATAGTCTG 372

QY 1063 TTGAATACATGCTGGAACCTACTATTGATGCTTTTATAATCCTTCTTAATACAGTTCTAA 1122
DB 373 TTGATATCAAGCTGGAACGACGCTACAGTTTACTATATATCCCGCAATACAGTACTTA 432
QY 1123 CTGGAAGCAGAGGTTTGGTTTCAGATGTTCTTTAATGTTGGATGATATCCAGGTGGG 1182
DB 433 ATGGTAAACCTGAAATTTGGTTTCAATGTTTCAATTTAATCGCTGGACTCACCGCTGGGTC 492
QY 1183 TGTTCGCCCTCAGAGATGTTTACAGAGAAATGGTTTACACCTTAAAGCAACAGTTT 1242
DB 493 CATTCGCCCTCAGAAATGTTCCGCTGCTGAAATGGCAACCATGTCAGAGCAATGTGA 552
QY 1243 AGTTTCCAGAGATGCTATATGATGGAATTCGTTTCTCGAGTCAAGAAAGGTGGAA 1302
DB 553 AGTTTCCATGATGATATGATGGAATTTGTTTCCAGAGAGAGATGTTGGGA 612
QY 1303 TTTATGATAACAGAAATGGTTAGACTATCATATTCCTGTTTGGTTCGAATGCAAAAGG 1362
DB 613 TTTTTCACAAATGAAGCGGAATGGACTATCATATCCTGTTTGGAGGAGTCGCTAAAG 672
QY 1363 AACCACTATGACATTTGTCACATTTGCTGTTGAGATGCAACCAATCGCAAGGTTGGAG 1422
DB 673 AACCTCAATGCAATTTGCTGCTGCAATGGCAATGGCAATTTGCAAGGTTGGAG 732
QY 1423 GCTTGGTGAATGTTGCTACTAGTCTTTTCACTGCTGCTGCAAGATTTAGGACACAATGTGG 1482
DB 733 GCTTGGTGAATGTTGCTACTAGTCTTTTCCGCTGCTGCTCAAGATTTAAACCATATGTGG 792
QY 1483 AGTTTATTTTCCAAAGTACGTTTCTGTAATCTAAGCAATGTCAAGATCTCAAAATCC 1542
DB 793 ATATTATCTTACCAATGATGACTGTTTGAAGATGAATAATGTAAGGACTTTTCGGTTTC 852
QY 1543 ATCAGAGTTTCTTGGGCTGCTGCTGAAATAAATGTTGGGCTGCACTAGTCGAAGGCC 1602
DB 853 ACATAAATCTACTTTTGGGCTGCACTGAAATGAAGTATGTTTGGAAAGGTTGGAAGTTC 912
QY 1603 TTTGTTTACTTCTCGAAGCTCAAAATGGGATGTTTGGATCGGATATGTAATG--- 1659
DB 913 TCTCGTCTATTTTGGAGCTCAAAACGGGTTATTTTGAAGAGGTCGCTATGTT 972
QY 1660 CGAGGAGATGACCGCGATTTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1719
DB 973 GTAGCAATGATGTTGAAAGATTTGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1032
QY 1720 AAAGTGAATCTTCTCGAAGCTCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1779
DB 1033 AAAGTGAATTTAGTCCGATATCATTCATTCGATGTTGTTTCTGCTGCTGCTGCTGCT 1092
QY 1780 GGCTACAGAGAAACTACGGAAGTCTAGTTGGCAAGCAGCGGTGTTTACCA 1839
DB 1093 GGCTCTTTAAGGAACAATATACACTATGTTTGAAGCAATCTCGTATAGTCTTCA 1152
QY 1840 TCCCAATCTTGAATTTGAGCGGATCATATTTGCAAGCAATGAGATTTGTAATGAAG 1899
DB 1153 TACATACTTTGAATTTGGGAGATCTCATTTGGAGAGCAATGACTAAGCAGACAAAG 1212
QY 1900 CAACAATGCTCTTAATACATATTTCAAGAGAGTGTGAGTGTGCTGCTGCTGCTGCT 1959
DB 1213 CTACAAGATTTTCAACAATTTACTACAGAGGTTCTGGAACCTGTAATTTGGGCTTC 1272
QY 1960 ATCTTGGGAATTTATGCGAATCTCAATGGAATGATTCGGAATATATGGGATCGGTACA 2019
DB 1273 ACCTTCAAGATTTTCAAGATTTAGTGAATGGAATTTGACCAAGATTTTGGGATCTTTAA 1332
QY 2020 ATGCAACTTTATCCGCTTCACTACATCTGTAAGATGTTGTAAGGCAAGGCGGTG 2079
DB 1333 ACGTAAAGTTTCACTCCGATTCGTTACACTCAGAAACGTTTGTGAAGCAAAACAGCAG 1392
QY 2080 CTAAAGAGGCTCTGAGAGAGGTTTGGGTTTACAGAAATGATGCTCCCGCTCGTAGGAA 2139
DB 1393 CCAAGGAAGCTTTGAGCGGAAACTTGGACTCAACAGGCTGACCTTCTTTTGGTAGGAA 1452
QY 2140 TCGTACTCGCTGACAGCCCAAAAGGGATGCCCTGATCAAGCATGCGATTCACCGTA 2199

DB 1453 TTATCACCGCTTAACTACAGAAAGAAATCCACCTCATTTAAACATGCTATTTTGGCGCA 1512
QY 2200 CACTCGAAGCAAGCAGAGTGGTTTGTGTTGTTTTCAGCGCCGAGCTCTCGAATCCAAAG 2259
DB 1513 CTTTGAACGCAAGCAGAGTGGTTTGTGTTGTTTCTGCTCTGCTAGGTACAAA 1572
QY 2260 CTGATTTTGTCAACTGCGGATAGCTTCCAGGGGTAAACCATGGGCAAGTGAAGCTTT 2319
DB 1573 ACGATTTTGTAAATTTGGCAATCAATTTGCACTCCAAATATAATGACCGGACGACTCT 1632
QY 2320 CTTGACCTACAGAGGCTCTCTCGCATCTGATATAGCTGGCTCTGACTTCACTTCTGG 2379
DB 1633 GTCTAACATATGACGAGCCTTTCTACCTGATATATGCTGGTCTGATTTTATCTAG 1692
QY 2380 TCCCATCTATATTTGAGCTTTCGCGCTTAACTAGCTCGTCCCATCGGCTATGGAACCA 2439
DB 1693 TCCCTTCAATATTTGAGCCTATGTGACTTAAACCACTTACCGCTATGAGATATGTTCAA 1752
QY 2440 TCCGATTTGTCGCAAGACTCGAGGCTCTTTCGACACTGCTTTCGATGTGCAATGACA 2499
DB 1753 TCCAGTCTGCTGTAATAACTGGAGACTTTATGATCTGTTGATGTTGACCAATGACA 1812
QY 2500 AGGAACGAGCCGAGATCGAGGCTTTCAGCCCAACGGGTTTTCAGCGAGCTGATA 2559
DB 1813 AAGAGAGACACACAGTGTGCTTTCGACCAATGATGATTCAGCTTTCAGTTCGAGCAGATG 1872
QY 2560 GCAACGGTGTGACTACGCGCTGAAACGAGGCGATCTCAG 2598
DB 1873 CTGGCGGAGTTGATTTGCTCTGATAGCTCTCTCTG 1911

RESULT 7

US-09-606-304-1

; Sequence 1, Application US/09606304

; Patent No. 6483010

; GENERAL INFORMATION:

; APPLICANT: Kossmann, Jens

; Springer, Franziska

; Abel, Gernot

; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES

; INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC

; PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FISH & NEAVE

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10020

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/606,304

; FILING DATE: 28-Jun-2000

; CLASSIFICATION: <Unknown>

; APPLICATION DATA:

; APPLICATION NUMBER: 08/836,567

; FILING DATE: 10-NOV-1994

; APPLICATION NUMBER: DE P 44 41 408.0

; FILING DATE: 10-NOV-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Haley Jr., James F.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: Agrevo-4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-596-9090

; TELEFAX: 212-596-9090

; INFORMATION FOR SEQ ID NO: 1:

```
;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 2303 base pairs
;   TYPE: nucleotide
;   STRANDEDNESS: unknown
;   TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
;   ORGANISM: Solanum tuberosum
;   STRAIN: cv Berolina
;   TISSUE TYPE: tuber tissue
; IMMEDIATE SOURCE:
;   LIBRARY: cDNA-library in pBluescriptSKII+
;   OTHER INFORMATION: CDS
; FEATURE:
;   LOCATION: 3..2033
;   OTHER INFORMATION: /function= "Polymerization of starch"
;   /product= "Starch synthase"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-606-304-1

Query Match      35.8%; Score 931; DB 4; Length 2303;
Best Local Similarity 68.5%; Pred. No. 2.2e-284;
Matches 1301; Conservative 0; Mismatches 595; Indels 3; Gaps 1;

QY 703 AAAGGCTGTTTCATCATCATGACAAAGATGTGATTTGGTGGTTTGCAGATGTTGCGTGC 762
DB 13 AAAAGCTTGTAAATCTGAGAAATAGATGGTGGTGGTATACAGAGGTTGTTATTC 72

QY 763 CTGAAGAACAATATGATTGGACTGGGTTTTCCTGACGGCCCAACAGGAGTGCAGGA 822
DB 73 CTGATCAGGCACTTTCITGGATTGGTTTTCCTGATGTTCCACCCAGCATGCCATG 132

QY 823 ATTATGACAAATGAGGAGCAATGATTTTCATGCTACCCCTTCCAAATAACATGACTGAGG 882
DB 133 CTTATGATAACAATCACGCCAAGACTTCCATGCCATTGTCGCCAACCAATTCGGGAGG 192

QY 883 AAGAGTATTGGATGAGAGAGCAACAAAGATCTATACAGGCTTCAACAGAGAGAGGG 942
DB 193 AATTATATTGGTTGAGGAGAAACATCAGATCTTAAAGACATTCAGGAGGAGAGAGGC 252

QY 943 AAAGGAGGAGGCTATTAAAGAGAGGCTGAGAGAAATGCAAAAATGAAAGCTGAGATGA 1002
DB 253 TTAGAGAGCGCTATGCGTGCTAAGGTTGAAATAACAGCACTTCTGAAATCTGAAACAA 312

QY 1003 AGGAAAGACTATGAGATGTTCCCTGGTTTCTCAGAAACACATTTGTTACCCGAAACAC 1062
DB 313 AGGAAAGAACTATGAAATCATTTTACTGTCTCAGAAAGCATGTAGTATATATCTGAGCCTC 372

QY 1063 TTGAAATACATGCTGGAATCTATTGATGCTTTTATAATCCTTCTAATACAGTTCTAA 1122
DB 373 TTGATATCAAGCTGGAAGCAGCGTCACAGTTTACTAATCCCGCAATACAGTACTTA 432

QY 1123 CTGAAAGCCAGAGTTGGTTTCGATGTTTCCTTTAATCGTTGGATGATCCAGGTGGGG 1182
DB 433 ATGGTAAACCTGAATTTGGTTTCAGATGTTTCATTTAATCGCTGGACTCACCCCTGGGTC 492

QY 1183 TGTTCGCACCTCAGAAGATGGTACAGAGAGAAATGGTTTCAACCTAAAGCAACAGTTT 1242
DB 493 CATTCGCCACCTCAGAAATGTGCGCTGCTGAAATGGCACCCATGTCAGAGCAACTGTGA 552

QY 1243 ACGTTCCAGCATGCTATATGATGGACTTCGTTTCTCGAGTCAGAGAGAGGTGGAA 1302
DB 553 AGGTTCCATGGATGCATATATATGATGATTTGTTATTTCCAGAGAGAAATGTTGGGA 612

QY 1303 TTTATGATAACAAATGGGTTAGACTATCAATTCCTGTTTTCCTGGTTCAATTCGAAAGG 1362
DB 613 TTTTGTGACAAATAGAGCGGAATGGACTATCATACTCTGTGTTTGGAGGAGTCGCTAAG 672

QY 1363 AACCACTATGACATTTGCCATTTGCTGTTGAGATGCGCAACATCGCAAAAGGTTGGAG 1422
DB 673 AACCTCCATGATATTGTCCATATTGCTGTGCAATGTCGCAATGCAACCAATTCGAAAGGTTGGAG 732
```

```
QY 1423 GTCTTGTTGATGTTGTTCTACTAGTCTTTTACGTCGTGTCGAAAGATTAGACACAATGTGG 1482
DB 733 GCCITGGTGATGTTGTTTACTAGTCTTTCCCGTGCTGTTCAAGATTAAACCAATATGTGG 792

QY 1483 AGGTTATTCTTCCAAAGTACGGTTGCTTGAATCTAAGCAATGTCAAGAAATCTACAAATCC 1542
DB 793 ATATTATCTTACCTAAGTATGACTGCTTTTGAAGATGAATAATGTGAAGGACTTTCGGTTTC 852

QY 1543 ATCAGAGTTTTCCTGGGTTGTTCTGAAATAAATGTTGTGGCGTGAGCTAGTCGAAGGCC 1602
DB 853 ACAAAAAATCTACTTTTGGGTTGGGACTGAAATAAAGATATGTTTGGAAAGGTGGAAGGTC 912

QY 1603 TTTTGTGTTTACTTCTCTGGAACCTCAAAATGGATGTTTGGAGTCGATATGATATG--- 1659
DB 913 TCTCGGTCTATTTTGGAGGCTCAAAACGGGTTATTTTCGAAAGGTCGCTATGTT 972

QY 1660 GCAGGAGCATGACCGCGGATTGGCTTCTTCTGTCGTTCTGCTCTAGAGTTTCTCTCC 1719
DB 973 GTAGCAATGATGGTGAAACGATTTGGTTTCTTCTGTCACGGGCTTGGAGTTTCTTCTCC 1032

QY 1720 AAGTGGATCTTCTCCGAAACATATAATTTGCCATGATTTGGTCAAGTCTCTCTGTTGCT 1779
DB 1033 AAGTGGATTTAGTCCGGATATCATTTGTCATTTGCCATGATTTGGTCTAGTCTCTCTGTTGCT 1092

QY 1780 GGCTACACAGGAAACTACGCGAAGTCTAGCTTGGCAACGACGCGGTGTTATTCACA 1839
DB 1093 GGCTCTTTAAGGAACAATATACACTATGGTCTAAGCAAAATCTCGTATAGTCTTACAGA 1152

QY 1840 TCCCAATCTTGAATTTGGAGCGCATCATATTGGCAAAAGCAATGAGATATTGTGATAAG 1899
DB 1153 TACATAATCTTGAATTTGGGCGAGATCTCATTTGGGAGAGCAATGACTAACGCAGACAAG 1212

QY 1900 CAAACACTGCTCTAATACATATTCAAAGGAAGTGTCAAGTCAATGGTCCATAGTTCTCTC 1959
DB 1213 CTACAACAGTTTCAACAACTTACTCACAGGAGGTGTCTGGAAACCTGTAAATTTGGCCTC 1272

QY 1960 ATCTTGGGAATTTCTATGCAATCTCAATGGAATTTCCGATATCCGATATATGGATCCGTACA 2019
DB 1273 ACCTTCAAGATTTCCATGGTATGTAATGGATTTGACCCAGATATTTGGGATCCCTTTAA 1332

QY 2020 ATGACAACTTATCCCGGTCCACTACACTTGTGAGAATGTGTTGAAAGCAAGAGGGCTG 2079
DB 1333 ACGATAAGTTTCATTCGGATTCGTACACCTCAGAAACAGTTGTTTGAAGCAAAACAGCAG 1392

QY 2080 CTAAGAGGCACTGACAGCAGAAAGTTGGTTTACAGCAATCGATGTCCTGCTAGTACAA 2139
DB 1393 CCAAGGAAGCTTTGACGCGAAACCTTGGACTGAAACAGGCTGACCTTCTCTTTGGTAGGAA 1452

QY 2140 TCGTCACCTCGCTGACAGCCCAAAAGGGATCCACCTGATCAAGCATGCGATTCCCGTAA 2199
DB 1453 TTATCACCCGCTTAACTCACAGAAAGGAATCCACTCATTTAAACATGCTATTTTGGCGCA 1512

QY 2200 CACTCGAACGGAACGACAGGTGGTTTGTGTTTTCAGCGCGGAGCTCTCGAATCCCAAG 2259
DB 1513 COTTGGAACGGAACGACAGGTAGTCTTGTGTTGTTGTTCTGCTCTGATCTTAGGTTACAA 1572

QY 2260 CTGATTTGTCAACCTCGCGAATACGCTCCACGGGTAAACCATGGGCAAGTAGGCTTT 2319
DB 1573 ACGATTTTGTAAATTTGGCAATCAATTTGCACTCCAAATATAATGACCGCGCAGCACTCT 1632

QY 2320 CTTTGACCTCAGAGAGCTCTCTCGCATCTGATATACGCTGGCTCTCACTTCACTTCGG 2379
DB 1633 GTCTAACATATGACAGAGCACTTCTCACCTGATATATGCTGGTGTCTGATTTTATCTAG 1692

QY 2380 TCCCATCTATATTTAGCCTTTGCGGCTTAACCTAGCTCGTCCCATCGGATGGAACCA 2439
DB 1693 TTCTTCAATATTTGAGCCATGTGAGCTAAACAACTTACCGCTATGAGATATGTTCAA 1752

QY 2440 TCCCGATTGTCGCAAGACTGAGGCTCTTCGACACTGTCTTCGATGTGACAAATGACA 2499
DB 1753 TTCCAGTCTGCGTAAACCTGAGGACTTTATGATACTGTATTTGATGTTGACCATGACA 1812
```

QY	2500	AGGAA CGAGCCCGAGATCGAGGCTT	TGAGCCCAACGGGTTT	TAGCTTTGACGGAGCTGATA	2559
Db	1813	AAGAGAGAGCACAAACAGTGTGGTCTT	TGAACCAATGGATT	CAGCTTTGATGGAGCAGATG	1872
QY	2560	GCAACGGTGTGACTACGCGCTGAACAGGCGCATCTCAG			2598
Db	1873	CTGCGGAGTGTGATTATGCTCTGAATAGAGCTCTCTCTG			1911

QY 2129 CGTCGTAGGAATCGTCACTCGCTGACAGCCCAAGGGGATCCACTGATCAAGCATGC 2188
Db 1628 ATTAGTTGGTTGCATACGAGGCTAGTTCTCAAAGGGGTGATCATCTCATCAGGCATGC 1687
QY 2189 GATTCCCGTACACTCGAAACGACAGGAGTGGTTTCTGTTGGTTTCAGCGCGGCACTC 2248
Db 1688 AATATATAAATAAATACTGAGTTGGGTGTCAATTTGTTCTGCTGGTTTCAAGTCCAGTACA 1747
QY 2249 TCGAATCCAGCTGATTTCTCACTCGGGAATACGCTCCAGGGGTAAACATGGGCA 2308
Db 1748 GCATATCCAGAGAGT-----CGAGGGTATTCGGGACCAATTTTCAGAACACACAA 1801
QY 2309 AGTGAGGCTTTCCTTGACCTACGACGAGCTCTCTGCACTGATATACGCTGCTCTGA 2368
Db 1802 TGTCAGGCTCTTTTGAAGTATGATGCTCTGGACATATATCTTTGCAGATCAGA 1861
QY 2369 CTTCAATTCCTGCTCCATCTATATTGAGCCTTGGGCTTAACCTCAGCTCGTCCCATGCG 2428
Db 1862 CATGTTCAATTTCTTCTATGTTTGAACCATGTGGCTCACTCAGATGTAGTATGCG 1921
QY 2429 GTATGGAACCATCCGATGCTCGCAGACTGAGGGCTCTTCGACACTCTCTTCATGT 2488
Db 1922 ATATGGTCTGTGCCAGTGTTCGGAGAACCGGCGTTTGAATGACAGTGTCTTCGATTT 1981
QY 2489 GGCAATGACAAAGAAC 2505
Db 1982 GGAAGATGAACGATAC 1998
RESULT 10
US-09-780-115-1
; Sequence 1, Application US/09780115
; Patent No. 6617495
; GENERAL INFORMATION:
; APPLICANT: Kossmann, Jens
; APPLICANT: Proberg, Claus
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES FROM PLANTS CODING ENZYMES
; TITLE OF INVENTION: WHICH PARTICIPATE IN THE STARCH SYNTHESIS
; FILE REFERENCE: GFB-6 DIV
; CURRENT APPLICATION NUMBER: US/09/780,115
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 09/115,704
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: PCT/EP97/00158
; PRIOR FILING DATE: 1997-01-15
; PRIOR APPLICATION NUMBER: DE 196 01 365.8
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2652
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9)..(2213)
US-09-780-115-1
Query Match 5.6%; Score 145; DB 4; Length 2652;
Best Local Similarity 51.4%; Pred. No. 5.2e-35;
Matches 657; Conservative 0; Mismatches 470; Indels 150; Gaps 8;
QY 1370 TATGCAATGTCCACATGCTGTTGATGATGGCACCACCAATCGCAAGGTTGGAGGCTTGG 1429
Db 731 TTGACATTTGCCATAGCAGAGATGGCTCTCGCAAGGTTGGGTGCTGCG 790
QY 1430 TGAGTGTCACTAGTCTTTCAGTCTGTCGAAGATTTAGGACACAAATGTGGAGTTAT 1489
Db 791 AGATGTGATCTGTGCTTGGGAAGGCACTTCAAAAAGGGGACCTTTGTAGAGATTAT 850
QY 1490 TCTTCCAAAGTAGGTTGCTTGAATTAAGCAATGTCAAGATCTTACAAATCCATCAGAG 1549

Db 851 TCTTCCAAATATGATTCATGATGAGCAGATACCAATAAATAATCTTAAGGTTCTAGATGT 910
QY 1550 TTTTCTTGGGGTGGTTCTGAAAATAAATGT-----TGGGGTGGACTAGT 1594
Db 911 TGTGGTGAAGTCTTACTTTGAAGGAAATATGTTTGCACAAAGATATGGACTGGAACGT 970
QY 1595 CGAAGCCCTTGTGTTTACTTCTCGAACCCTCAAAA-----TGGGATGTTTGGAGTCGG 1648
Db 971 TGAAGTCTTCCGGTCTTACTTTTGAACCGCAACATCCAGGTAAGTCTTCTTGGAGGGC 1030
QY 1649 ATATGTATATGCGAGGAGCATGACCGC---CGAATTGGCTTCTCTGTCGTTCTGCTCT 1705
Db 1031 ACATATCTACGAGAGCATGATGACTTCAACGTTTTTGTACTTTAGCGGTGTGACT 1090
QY 1706 AGAGTTCTCTCCAAAGTGGATCTTCTCGAACAATAATCAATTCGATGATGATGGTCAAG 1765
Db 1091 GGAATTGCTTTTACCAATCTGGGAAGAAAGTTGACATAATTCATGCTGCTGACTGGCAGAC 1150
QY 1766 TGCTCTGTTGCTGCTGCTACCAAGGAAACACTACGGAAGTCTAGCTTGGCAACGCAAG 1825
Db 1151 TGAATTTGTTGACCTCTTTTACTGGGATGTATATGCAAACTGGGCTTCAACTCAGCTAG 1210
QY 1826 GGTGTATTTCACCATCCACAATCTTGAATTT-----1856
Db 1211 AATTTGTTTACTGTCACAAATTTGAATATCAAGGAATCGCTCCAGCTCAGACTAGC 1270
QY 1857 -----1856
Db 1271 ATATTGTGCTTGTATGTTGATCACCCTGGATAGACACAGAAATCGGGATAATTCACA 1330
QY 1857 ---GGAGCGCATCATATTGGCAAGCAATGAGATATTCTGATAAAGCAACACTGCTC 1912
Db 1331 TGGCAGAAATAATGTTGTTAAGGTGCAAGTTGATATTTCCAACTTGTGCAACTGTATC 1390
QY 1913 TAATACATATCAAGGAAAGTGTCAAGTCTATGTTGCTATGTTCCCTCATCTT-----1964
Db 1391 ACCAATATGACAAAGAGTTCGCTCAGAGGTGGCGCTCCAGATACACTCA 1450
QY 1965 -----GGGAATTTCTATGGCAATTCATGGAATGTATGATATATGGATCC 2014
Db 1451 AGTGCACTCCAAAGAAATTTGTTGGAATACTTAATGCAATTGACACAGATATCTTGAATCC 1510
QY 2015 GTACATGACAACTTTATCCCGTCCACTACACTGTTGAGAAATGTTGTAAGGCAAGAG 2074
Db 1511 GTCTACGGATAGTTTCTCAAGTTCAATACA---GTGCTAATGATCTATATGGAAGTC 1567
QY 2075 GGTGCTAAGAGGGCACT-----GCAGCAGAAGTTTGGGTTACAGCAAAATCGATGCTCC 2128
Db 1568 AGCAAAACAAAGCAGCTCTTAGGAAGCAGTTGAAGCTTGTCTCCACACAAAGCTTCTCAAC 1627
QY 2129 CGTGTAGGAATCGTCACTCGCTGACAGCCCAAGGGGATCCACCTGATCAAGCATGC 2188
Db 1628 ATTAGTTGGTTGCTATACGAGGCTAGTTCTCTCAAAAGGGGTGATCATCTCATCAGGATGC 1687
QY 2189 GATTCAACGCTACACTCGAACGGAACGACAGTGGTTTGTGTTGTTGTTGTTGTTGTTGTTG 2248
Db 1688 AATATATAAATAACTAGTGGTGGTTCATTTGTTCTGCTGGGTTCAAGTCCAGTACA 1747
QY 2249 TCGAATCCAAAGCTGATTTTGTCAACCTGGCGAATACGCTCCACGGCGTAAACCATGGGCA 2308
Db 1748 GCATATCCAGAGAGAGT-----CGAGGGTATTCGGGACCAATTTTCAGAAACAAACAA 1801
QY 2309 AGTGGGCTTCTTTCAGCTAGCAGGCTCTCTCGGATCTGATATAGCTTGGTGTCTGA 2368
Db 1802 TGTGAGGCTGCTTTTGAAGTATGATGCTCTGGCACAATATGATCTTTGACAGCATCAGA 1861
QY 2369 CTTCAATCTGGTCCCATCTATATTTGAGCTTGGCGCTTAAGTCTAGCTGCTGCCATGCG 2428
Db 1862 CATGTTCAATGTTCTTCTATGTTTGAACATGTGGCTCTACTCAGATGTTAGTATGG 1921
QY 2429 GTATGGAACCATCCGATGTTGCGCAAGACTGGAGGGCTCTTCGACACTGTCTTCGATGT 2488
Db 1922 ATATGGTCTGTGCCAGTGTTCGGAGAACCGGCGTTTGAATGACAGTGTCTTCGATTT 1981

Db 522 CAAAGCATCTGCTGCTGCGGATGCGCTACGCTACGACACGCTGAGGAGAGCGGAG 463
QY 2076 GCTGCTAAGAGGCACTGACGACGAGAGTTGGTTACACGAATCGATCTCCCGTCGTA 2135
Db 462 AACAAAGCGTCAGCTGCAGATTCGATGGGCGCTGAAGGTCGATGAAGCGCGTTGTTT 403
QY 2136 GGAATCGTCACTCGCTGACGCCCAAAAGGGGATCCACTGATCAAGCATCGATTAC 2195
Db 402 GCGCTGCTGACGCTGTTACAGCCAGAAAGGCTGGACCTGGTGTCTTGAAGCGCTGCCG 343
QY 2196 CGPACACTGAACGGAACGAGAGGTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTT 2255
Db 342 GGTCTGCTTGGACAGGCGGCCAGCTGGGCGCTGCTGGGCGCGCGCATCGGTCGTCAG 283
QY 2256 CAAGCTGATTTGTCACCTGGCGATACGCTCCACGGGCTAAACCATGGCAAGTGAGG 2315
Db 282 GAAGTTTCTTGCGCG-----CGCGCGCGGAACACCGCGGCGCAAGTGCGT 238
QY 2316 CTTTCCTTGACCTACGACGAGCCTCTCTGCACTCTGATATACGCTGGCTCTGACTTCATT 2375
Db 237 GTCAGATTGGCTACCATGAGGCTTCTCCACCGCATTTATGGCGCGCGCGACGTCATT 178
QY 2376 CTGGTCCCATCTATATTGAGCCTTGGCGCTTAACCTCAGCTCGTGGCCATGCGGTATGA 2435
Db 177 CTGGTCCGAGCGCTTTGAAACCTCGGCGCTGACCCAGCTGTATGGTCTGAAGTACGGG 118
QY 2436 ACCATCCGATGTCGCGAAGCTGGAGGCTCTTCGACACTGTCTTGA 2485
Db 117 ACCTGCGCTGGTGGCGCGACCGCGGCTGGCGGACACCGTCGCTGA 68

RESULT 15

US-09-489-039A-3862

; Sequence 3862, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 3862

; LENGTH: 1536

; TYPE: DNA

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-3862

Query Match 3.2%; Score 83.6; DB 4; Length 1536;
Best Local Similarity 49.2%; Pred. No. 1e-15;
Matches 261; Conservative 0; Mismatches 254; Indels 15; Gaps 1;
QY 1956 COTCATCTTTGGGAATTTCTATGTCATCTCAATGGAATTCATCCGGATATATGGATCCG 2015
Db 808 CATCATGAAGTCCGCTGTCGGGAATTCACAGGGGTTGACGACGGTATCTGGAGCCCG 867
QY 2016 TACATGACAACTTTATCCGGTCCACTACCTTGTGAGATGTGTTGAAGGCAAGAGG 2075
Db 868 CAAACGATCTGCTGCTGCGGATCGCTACGATCGCGACACGCTGGAGGAGAAGCGGAG 927
QY 2076 GCTGCTAAGAGGSCACTGACGACGAGATTGGGTTACAGCAATCGATGCCCGTCGTA 2135
Db 928 AACACGGTCAGCTGAGATTCGCATGGGCTGAAGTCGATGAATAAGCCGTTGTTT 987
QY 2136 GGAATCGTCACCTGCGCTGACAGCCCAAAAGGGGATCCACTGATCAAGCATGCGATTAC 2195
Db 988 GCGTCTGTCAGCGCTCTTACACGACCAAGAGGCTGGAACCTGGTGTCTTGAAGCGCTGCCG 1047
QY 2196 CGTACACTGAACGGAACGAGCAGGTGGTTTTCGTTGTTTACGCGCGGACTCTCGAATC 2255

Db 1048 GGTCTGCTTGAGCAGGCGGCCAGCTGGGCTGCTGGGCGCGCGGATCCGGTGTGCGAG 1107
QY 2256 CAAGCTGATTTTGTCAACCTGGCGAATACGCTCCACGGCGTAACCATGGGCAAGTGAGG 2315
Db 1108 GAAGTTTCTTTCGCGG-----CCGCGCGCGGAACACCCCGGGCAAGTGGGT 1152
QY 2316 CTTTCCTTGACCTACGACGAGCCTCTCTGCACTCTGATATACGCTGGCTCTGACTTCATT 2375
Db 1153 GTGCGAGATTGGCTACATGAGGCTTCTCCACCGCATTTATGGGCGCGCGCGACGTCATT 1212
QY 2376 CTGGTCCCATCTATATTGAGCCTTTCGGGCTTAACCTCAGCTCGTCCCATGCGGTATGA 2435
Db 1213 CTGGTCCCGAGCGGCTTTGAACCTTCGGGCTGACCCAGCTGTATGGTCTGAAGTACGGG 1272
QY 2436 ACCATCCGATTTGTCGCAAGACTGGAGGCTCTTCGACACTGTCTTGA 2485
Db 1273 ACGTGGCGCTGGTGGCGCGCACCGCGGCTCTGGCGGACACCGTCGCTGA 1322

Search completed: June 20, 2004, 12:54:58

Job time : 222 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 20, 2004, 05:15:45 ; Search time 1495 Seconds

(without alignments)
7960.983 Million cell updates/sec

Title: US-10-634-262-1_COPY_2425_5022

Perfect score: 2598

Sequence: 1 agctgtctgaaaaaattat.....gtgaacaggcgatctcag 2598

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/prodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/prodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/prodata/2/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/prodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/prodata/2/pubpna/US09_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
- 15: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
- 16: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
- 17: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2598	100.0	6027	13	US-10-634-262-1
2	2598	100.0	6027	17	US-10-109-048-1145
3	1204.8	46.4	3693	15	US-10-424-799-1
4	1204.8	46.4	4168	15	US-10-284-668-11
5	931	35.8	2303	15	US-10-284-668-1
6	924.8	35.6	1338	13	US-10-425-114-20351
7	826.4	31.8	2581	13	US-10-425-114-30909
8	724.4	27.9	2218	13	US-10-424-599-97896
9	480.4	18.5	1181	13	US-10-425-114-4321
10	315.8	12.2	585	16	US-10-341-961A-91
11	290.6	11.2	548	9	US-09-739-438-3
12	283.8	10.9	641	13	US-10-424-599-83485
13	207.6	8.0	437	9	US-09-739-438-1
14	186.2	7.2	464	13	US-10-424-599-84418

Sequence 3346, Ap
Sequence 3520, Ap
Sequence 109987,
Sequence 33865, A
Sequence 1, Appli
Sequence 9, Appli
Sequence 11, Appli
Sequence 3300, Ap
Sequence 5, Appli
Sequence 33677, A
Sequence 29678, A
Sequence 29680, A
Sequence 42704, A
Sequence 14355, A
Sequence 33675, A
Sequence 35219, A
Sequence 46953, A
Sequence 8641, Ap
Sequence 3, Appli
Sequence 64934, A
Sequence 44603, A
Sequence 35062, A
Sequence 38466, A
Sequence 38620, A
Sequence 38957, A
Sequence 31744, A
Sequence 1052, Ap
Sequence 48, Appli
Sequence 1144, Ap
Sequence 38452, A

9 US-09-294-093B-3346
9 US-09-294-093B-3520
13 US-10-424-599-109987
13 US-10-425-114-33865
15 US-10-163-214-1
15 US-10-044-543-9
15 US-10-163-214-9
15 US-10-163-214-11
15 US-09-294-093B-3300
15 US-10-163-214-5
15 US-10-163-214-5
16 US-10-369-493-33677
13 US-10-424-599-29678
13 US-10-424-599-29680
16 US-10-369-493-42704
16 US-10-425-114-14355
13 US-10-369-493-33675
16 US-10-369-493-35219
16 US-10-369-493-46953
13 US-10-425-114-8641
15 US-10-138-075-3
13 US-10-424-599-64934
16 US-10-369-493-44603
16 US-10-369-493-35062
16 US-10-369-493-38466
16 US-10-369-493-38620
16 US-10-369-493-38957
13 US-10-425-114-31744
13 US-10-425-114-1052
13 US-10-336-753-48
17 US-10-109-048-1144
16 US-10-369-493-38452

ALIGNMENTS

RESULT 1

US-10-634-262-1
; Sequence 1, Application US/10634262
; Publication No. US20040049810A1
; GENERAL INFORMATION:
; APPLICANT: Myers, Alan M.
; APPLICANT: James, Martha G.
; TITLE OF INVENTION: dulla Coding for a No. US20040049810A1 Starch Synthase and Uses
; TITLE OF INVENTION: Theroof
; FILE REFERENCE: D6036PCT
; CURRENT APPLICATION NUMBER: US/10/634,262
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: US/09/554,467A
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: PCT/US98/24225
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/062,102
; PRIOR FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 37
; SEQ ID NO 1
; LENGTH: 6027
; TYPE: DNA
; ORGANISM: maize
; FEATURE:
; OTHER INFORMATION: cdna sequence corresponding to the gene encoding the
; OTHER INFORMATION: starch synthase enzyme DUL.
US-10-634-262-1

Query Match 100.0%; Score 2598; DB 13; Length 6027;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGCTGAAAAAATTATTCGCTGGGAAACAACTGTTTACTTATCCAGATGTTTGA 60

DB 2425 AGCTGCTGAAAAAATTATTCGCTGGGAAACAACTGTTTACTTATCCAGATGTTTGA 2484

QY 61 AAGCTGATTCACAAATGTATCTCTATTTCATCGTGATCTATCAGCTGTGGCCAAATGAGC 120

Db	2485	AAGCTGATTCACCAATTTGATCTCTATTTCATCGTGACTATCAGCTGTGGCCAAATGAGC	2544
Qy	121	CTGATGTACTTATCAAAAGGACATTCATGGGTGGAAAGTGAGATTTTTTCACTGAAAAAT	180
Db	2545	CTGATGTACTTATCAAAAGGACATTCATGGGTGGAAAGTGAGATTTTTTCACTGAAAAAT	2604
Qy	181	TGCACAAAGAGGAGCTGGCAGGGGACGTGGTGGTCTGCAAACTATACATTCCTTAAGCAGG	240
Db	2605	TGCACAAAGAGGAGCTGGCAGGGGACGTGGTGGTCTGCAAACTATACATTCCTTAAGCAGG	2664
Qy	241	CATACAGAAATGGACTTTGTGTTTTTAAACGACACACGGTATATGAAAAATAAACAATA	300
Db	2665	CATACAGAAATGGACTTTGTGTTTTTAAACGACACACGGTATATGAAAAATAAACAATA	2724
Qy	301	ATGATTTCTGTGATACAAATGAAAGCCATGGATGAAAAATTTATTTGAGGATTTCTTTGG	360
Db	2725	ATGATTTCTGTGATACAAATGAAAGCCATGGATGAAAAATTTATTTGAGGATTTCTTTGG	2784
Qy	361	CTGAAGAAAAAGCAACGAGAACTTCAGAAACCTTGCAAATGAGGAGCTGAAAGGAGGAGAC	420
Db	2785	CTGAAGAAAAAGCAACGAGAACTTCAGAAACCTTGCAAATGAGGAGCTGAAAGGAGGAGAC	2844
Qy	421	AAACTGATGACAGCGCGCGAATGGAAGGAAGAAAGGCGCGCAGATAAAGCTGACAGGGTAC	480
Db	2845	AAACTGATGACAGCGCGCGAATGGAAGGAAGAAAGGCGCGCAGATAAAGCTGACAGGGTAC	2904
Qy	481	AAGCCAAAGTTGAGTGTAGACGAGGAAGAAATAATGTGCAATGTATCGGTATTCGGTTAGCCA	540
Db	2905	AAGCCAAAGTTGAGTGTAGACGAGGAAGAAATAATGTGCAATGTATTCGGTTAGCCA	2964
Qy	541	GAGCTCCTGTTGATTAATTTATGTTACATTTGAGCCCATCAGCTGGCAAGAGGCTACTG	600
Db	2965	GAGCTCCTGTTGATTAATTTATGTTACATTTGAGCCCATCAGCTGGCAAGAGGCTACTG	3024
Qy	601	TCGATTTGATTTAAACATAAACTCAGACCTCTAGTTTCACGTACTGAGATATGATGTC	660
Db	3025	TCGATTTGATTTAAACATAAACTCAGACCTCTAGTTTCACGTACTGAGATATGATGTC	3084
Qy	661	ATGTTGCTCATAAACATTTGATTGATGGAATCTCTTTTGTGAAAGGCTTTGTTCAATCATC	720
Db	3085	ATGTTGCTCATAAACATTTGATTGATGGAATCTCTTTTGTGAAAGGCTTTGTTCAATCATC	3144
Qy	721	ATGACAAAGATTTGATTTGGTGTTCGAGATGTTTGCCTGCTGAAAGAACATATGTAT	780
Db	3145	ATGACAAAGATTTGATTTGGTGTTCGAGATGTTTGCCTGCTGAAAGAACATATGTAT	3204
Qy	781	TGGAATGGGTTTTTGTCTGACGGGCCACGAGGAGTGCAAGGAATTTATGACAAACAATGGAG	840
Db	3205	TGGAATGGGTTTTTGTCTGACGGGCCACGAGGAGTGCAAGGAATTTATGACAAACAATGGAG	3264
Qy	841	GACATGATTTTCATGCTACCTTCCAAATAACATGACTGAGGAAGAGTATTTGATGGAAG	900
Db	3265	GACATGATTTTCATGCTACCTTCCAAATAACATGACTGAGGAAGAGTATTTGATGGAAG	3324
Qy	901	AAGAAACAAAGATCTATACAGGCTTCCAAAGAGAGGAGGAAAGGAGGAGGCTATTTA	960
Db	3325	AAGAAACAAAGATCTATACAGGCTTCCAAAGAGAGGAGGAAAGGAGGAGGCTATTTA	3384
Qy	961	AAAGGAAGGCTGAGAGAAATGCAAAAAATGAAAGCTGAGATGAAGGAAAAAGACTATGAGAA	1020
Db	3385	AAAGGAAGGCTGAGAGAAATGCAAAAAATGAAAGCTGAGATGAAGGAAAAAGACTATGAGAA	3444
Qy	1021	TGTTCTCTGTTTCTCAGAAACAGATTTTACACCGAACCACTTGAATACATCTCTGGAA	1080
Db	3445	TGTTCTCTGTTTCTCAGAAACAGATTTTACACCGAACCACTTGAATACATCTCTGGAA	3504
Qy	1081	CTACTATTGATGTCTTTATAATCCITCTAATAACAGTTCTAACTGGAAGCCACAGAGTTT	1140
Db	3505	CTACTATTGATGTCTTTATAATCCITCTAATAACAGTTCTAATAACAGTTCTAATACTGGAAGCCACAGAGTTT	3564
Qy	1141	GGTTTCGATGTTCTTTTAATTCGTTTGGATGATCCAGGTGGGGTGTGGCCACCTCAGAAGA	1200

2281 ATACGCTCCACGGCGTAAACCATGGCAAGTGGAGGCTTCTTGAACCTACGACGAGCCTC 2340
4705 ATACGCTCCACGGCGTAAACCATGGCAAGTGGAGGCTTCTTGAACCTACGACGAGCCTC 4764
2341 TCTCGCATCTGATATAGCTGGCTCTGACCTTCACTTCTGGTCCCATCTATATTTTGGCCCTT 2400
4765 TCTCGCATCTGATATAGCTGGCTCTGACCTTCACTTCTGGTCCCATCTATATTTTGGCCCTT 4824
2401 CGGCGCTTAACTCAGCTCGTCCCATCGGCTATGGAACCATCCCGATTTGTCCGCAAGACTG 2460
4825 CGGCGCTTAACTCAGCTCGTCCCATCGGCTATGGAACCATCCCGATTTGTCCGCAAGACTG 4884
2461 GAGGCTCTTTCGACACTGTCTTGATGTGACATGACAAAGAAAGCAAGCCCGAGATCGAG 2520
4885 GAGGCTCTTTCGACACTGTCTTGATGTGACATGACAAAGAAAGCAAGCCCGAGATCGAG 4944
2521 GCCTTGAGCCCAACGGGTTTGTAGCTTTGACGCGAGCTGATGACAAAGGTTGTGACTACGCGC 2580
4945 GCCTTGAGCCCAACGGGTTTGTAGCTTTGACGCGAGCTGATGACAAAGGTTGTGACTACGCGC 5004
2581 TGAACAGGGCGATCTCAG 2598
5005 TGAACAGGGCGATCTCAG 5022

RESULT 2
US-10-109-048-1145
; Sequence 1145, Application US/10109048
; Publication No. US20040107461A1
; GENERAL INFORMATION:
; APPLICANT: COMMURI, PADMA
; APPLICANT: KBEILING, PETER L.
; APPLICANT: RAMIREZ, NORA
; APPLICANT: MCKEAN, ANGELA
; APPLICANT: GAO, ZHONG
; APPLICANT: GUAN, HANPING
; TITLE OF INVENTION: GLUCAN CHAIN LENGTH DOMAINS
; FILE REFERENCE: 2461-76
; CURRENT APPLICATION NUMBER: US/10/109,048
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/279,720
; PRIOR FILING DATE: 04-01-2004
; NUMBER OF SEQ ID NOS: 1154
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1145
; LENGTH: 6027
; TYPE: DNA
; ORGANISM: Zea mays
US-10-109-048-1145

Query Match 100.0%; Score 2598; DB 17; Length 6027;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGCTTCTGTAAGAAATATTTCCTGGGAACCAAGTTGTTTACTTATCCAGATGTATTGA 60
2425 AGCTTCTGTAAGAAATATTTCCTGGGAACCAAGTTGTTTACTTATCCAGATGTATTGA 2484
61 AAGCTGATTCACAAATGATCTCTATTTCATCTGATCTATCAGCTGTGGCCCAATGAGC 120
2485 AAGCTGATTCACAAATGATCTCTATTTCATCTGATCTATCAGCTGTGGCCCAATGAGC 2544
121 CTGATGATCTTATCAAGAGGAGCTTCAATGGGTGGAAAGTGAGATTTTCACTGAAAT 180
2545 CTGATGATCTTATCAAGAGGAGCTTCAATGGGTGGAAAGTGAGATTTTCACTGAAAT 2604
181 TGCACAGAGGAGCTGCGAGGAGCTGTGGTCTGCAACTATATCATCTTCAAGCAGG 240
2605 TGCACAGAGGAGCTGCGAGGAGCTGTGGTCTGCAACTATATCATCTTCAAGCAGG 2664
241 CATACAGATGAGCTTGTGTTTAAACGACACACGAGTATATGAAATAATAACAATA 300

2665 CATACAGATGAGCTTGTGTTTAAACGACACACGGTATATGAAATAATAACAATA 2724
301 ATGATTTCTGTGATACAAATAGAAAGCACCATGATGAAATTTATTTGAGGATTTCTTGG 360
2725 ATGATTTCTGTGATACAAATAGAAAGCACCATGATGAAATTTATTTGAGGATTTCTTGG 2784
361 CTGAGAAAGCAAGCAAGAGAACTTGAGAACTTGCAATAGAGGAGCTGAAAGAGGAGAC 420
2785 CTGAGAAAGCAAGCAAGAGAACTTGAGAACTTGCAATAGAGGAGCTGAAAGAGGAGAC 2844
421 AACTCATGAGCAGCGCGGAAATGAGAGAAAGAGCGCGAGATAAGCTGACAGGATAC 480
2845 AACTCATGAGCAGCGCGGAAATGAGAGAAAGAGCGCGAGATAAGCTGACAGGATAC 2904
481 AAGCCCAAGGTTGAGGTTAGAGACGAAGAATAAATTTGTCAATGATTTGGGTTTAGCCA 540
2905 AAGCCCAAGGTTGAGGTTAGAGACGAAGAATAAATTTGTCAATGATTTGGGTTTAGCCA 2964
541 GAGCTCTGTGATATATTTATGATATGATGAGCCCATCAGACTGACCAAGAGGCTACTG 600
2965 GAGCTCTGTGATATATTTATGATATGATGAGCCCATCAGACTGACCAAGAGGCTACTG 3024
601 TCAGATTTGATTAATAACATAAACTCAAGACCTCTAGTTTACAGTACTGAGATGATGATGC 660
3025 TCAGATTTGATTAATAACATAAACTCAAGACCTCTAGTTTACAGTACTGAGATGATGATGC 3084
661 ATGGTGGCTATATAACAAATGGATGATGAGCTCTCTTTTGTGTAAGGCTTTTCAATC 720
3085 ATGGTGGCTATATAACAAATGGATGATGAGCTCTCTTTTGTGTAAGGCTTTTCAATC 3144
721 ATGACAAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
3145 ATGACAAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3204
781 TGGACTGGGTTTGTGCTGACGGCCACCAAGGAGTGCAGGAAATTTATGACAAATGGAG 840
3205 TGGACTGGGTTTGTGCTGACGGCCACCAAGGAGTGCAGGAAATTTATGACAAATGGAG 3264
841 GACATGATTTTCATGCTACCCCTTCCAAATGACATGATGAGGAGAGTATGATGATGATG 900
3265 GACATGATTTTCATGCTACCCCTTCCAAATGACATGATGAGGAGAGTATGATGATGATG 3324
901 AAGAACAAAGGATCTATACAGGCTTCAACAGAGAGGAGGAGGAGGAGGAGGAGGATTTA 960
3325 AAGAACAAAGGATCTATACAGGCTTCAACAGAGAGGAGGAGGAGGAGGAGGAGGATTTA 3384
961 AAGAGGAGGCTGAGAGAAATGCAAAATGAGATGAGAGGAGGAGGAGGAGGAGGAGGAGG 1020
3385 AAGAGGAGGCTGAGAGAAATGCAAAATGAGATGAGAGGAGGAGGAGGAGGAGGAGGAGG 3444
1021 TGTTCTGTTTCTCAGAAACACATTTTACACCGAACACATTTGAAATATACATGCTGGAA 1080
3445 TGTTCTGTTTCTCAGAAACACATTTTACACCGAACACATTTGAAATATACATGCTGGAA 3504
1081 CTACTATGATGCTTCTTATATCCCTTCTAATACAGTCTTAACTGGAAGGAGGAGGATTT 1140
3505 CTACTATGATGCTTCTTATATCCCTTCTAATACAGTCTTAACTGGAAGGAGGAGGATTT 3564
1141 GGTTTCGATGTTTCTTATATCCCTTCTAATACAGTCTTAACTGGAAGGAGGAGGATTT 1200
3565 GGTTTCGATGTTTCTTATATCCCTTCTAATACAGTCTTAACTGGAAGGAGGAGGATTT 3624
1201 TGTTCTGTTTCTCAGAAACACATTTTACACCGAACACATTTGAAATATACATGCTGGAA 1260
3625 TGTTCTGTTTCTCAGAAACACATTTTACACCGAACACATTTGAAATATACATGCTGGAA 3684
1261 ATATGATGACTTCTGTTTCTCGAGTCAAGAGAGTGGAAATTTATGATTAACAGAAATG 1320
3685 ATATGATGACTTCTGTTTCTCGAGTCAAGAGAGTGGAAATTTATGATTAACAGAAATG 3744
1321 GGTTAGACTATCATATTCCTGTTTGGGTCAATTTCAAGGAGGAGGAGGAGGAGGAGGAGG 1380
3745 GGTTAGACTATCATATTCCTGTTTGGGTCAATTTCAAGGAGGAGGAGGAGGAGGAGGAGG 3804

Sequence 11, Application US/10284668
Publication No. US20030106100A1
GENERAL INFORMATION:
APPLICANT: Kossmann, Jens
Springer, Franziska
Abel, Gernot
TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/284,668
FILING DATE: 29-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/836,567
FILING DATE: 24-JUL-1997
APPLICATION NUMBER: PCT/EP95/04415
FILING DATE: 09-NOV-1995
APPLICATION NUMBER: DE P 44 41 408.0
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Agrevo-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4168 base pairs
TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to RNA
ORIGINAL SOURCE:
ORGANISM: Solanum tuberosum
STRAIN: cv. Desire
TISSUE TYPE: leaf tissue
IMMEDIATE SOURCE:
LIBRARY: cDNA-library in Lambda ZAPII
FEATURE:
NAME/KEY: CDS
LOCATION: 307..3897
SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Query Match 46.4%; Score 1204.8; DB 15; Length 4168;

Best Local Similarity 66.7%; Pred. No. 0;

Matches 1735; Conservative 0; Mismatches 862; Indels 3; Gaps 1;

QY 2 GCCTGGTGAAGAAATTAATCGTGGGAAACAGTTCTTTACTATCCAGATGATGAA 61

Db 1176 GCTTGGCGAGAAATTAATGCAAGGATCAGATATTTTGTTCAGAGGTTGTAA 1235

QY 62 AGCTGATTCACAAATGATCTCTATTTCAATCGTATCTATCAGTGTGCGCCATGAGCC 121

Db 1236 ACCTGATGAGATCTCGAGATATTTCTTAACAGAGGTCITTCACITTTGAAGATGATC 1295

QY 122 TGATGTAATCAAGAGCATTCATGAGGTTGAGTGGAGATTTTCTACTGAAAT 181

Db	1296	TGATGCTTTGATTATGGGAGCTTTTATATGATGGGCGCTATAGTCTTTTACTACAAGGCT	1355
QY	182	GCACAAGAGCGAGCTGGCAGGAGACTGGTGGTCTGCGAAACTATACATCTCTPAACAGGC	241
Db	1356	AACTGAGACTCATCTCAATGGAGATTGGTGTCTTGAAGATCCATGTTCACAGGAAGC	1415
QY	242	ATACAGAATGACTTTGTGTTTTTAAACGACACACCGGTATATGAAATAATAACAAATAA	301
Db	1416	ATACAGGCTGATTTTGTGTTTTTAAATGGAACAAGATGCTATGACAACAATGATGGA	1475
QY	302	TGATTTCTGTGATACAAATAGAAAGCACCATGGATGAAAATTTTATTTGAGGATTTCTTGC	361
Db	1476	TGACTTCAGTATACTGTCAAAGGTGTATGCAAAATCATTTGACTTTTGAATAATTTCTTGT	1535
QY	362	TGAAGAAAGCAACGAGAACTTTGAAACCTTCCAAATGAGGAGCTGAAAGAGAGACA	421
Db	1536	TGAGGAGAAATGGAGAGAACAGAGGAAACTTGTCTAAAGAACCAAGCTGAAAGAGAA	1595
QY	422	AACTGATGAGCGCGCGAATGGAGAGAAAGGCGCGAGATAAAGCTGACAGGATACA	481
Db	1596	ACGGGAGAGAACAAAGACGATAGAGAGCAGAAAGCTGAAATTTGAAGCTGACAGAGACA	1655
QY	482	AGCCAAAGGTTGAGTAGAGACGAAAGAAATAAATTTGCAATGATTTGGGTTTACCCAG	541
Db	1656	AGCAAAAGGAAGAGGCTGCAAAAGAAAGAAAGATTTTGCAGAAATTTGATGTTAAAGCCAC	1715
QY	542	AGCTCCTGTTGATAATTTATGTCATATTGAGGCCATCAGACTGCGAAGAGGCTACTGT	601
Db	1716	GAGACTCGTGATATCACGTGTGATAGAGCAAGTGAATTTAAATGCGAGGACAAGT	1775
QY	602	CAGATTGATTATAACATAAACTCAAGACCTCTAGTTCACAGTACTGAGATATGATGCA	661
Db	1776	CAGGTTATATACAAAGTTTCAAGTCTCTCTCCCATGCTAAGGACTTCTGGATCCA	1835
QY	662	TGTTGGCTATAACAATTTGATGAGTGGACTCTCTTTTGTCTGAAAGCTTTGTTTCATCATCA	721
Db	1836	CGGAGGATATAAATTTGAAGAGTGTGTCTATTTGTCAAAAAGCTTTGTTAAATCTCA	1895
QY	722	TGACAAAGATTTGATTTGGTGGTTTGCAGATGTTCTCGTGCCCTGAAAGAACATATGATT	781
Db	1896	GAGAAATAGATGTTGATTTGGTGTATACAGAGTTGTTATTTCTGATCAGGCACTTTCTT	1955
QY	782	GGACTGGGTTTTTGTCTGACGGCCCAACAGGAGTCAAGGAATTTATGACAAATGGAG	841
Db	1956	GGATTTGGGTTTTTGTGATGTTCCACCCCAAGCATGCCATTGCTTATGATAAATCAACCG	2015
QY	842	ACATGATTTTCTATGCTACCCCTTCCAAATAACATGACTGAGGAGAGATTTGATGTAAGA	901
Db	2016	CCAAGACTTCCATGTCATTTGTCCTCCCAACCAATTCGGAGGAATTTATTTGGGTTGAGGA	2075
QY	902	AGAACAAAGGATCTATACAAAGCTTCAACAGAGAGGAGGAAAGGAGGAGGCTATTAA	961
Db	2076	AGAACATCAGATCTTTAAGACACTTCAGAGGAGAGAGGCTTAGAGAGCGGCTATGCG	2135
QY	962	AAGGAGGCTGAGAGAAATGCAAAATGAAAGCTGAGATGAAAGGAAAGAAAGACTATGAGAAT	1021
Db	2136	TGCTAAGGTTGAAAGAAACAGCACTTCTGAAACTGAAACAAAGGAAAGAACTATGAAATC	2195
QY	1022	GTTCTCGGTTTCTCAGAAACACATTTGTTTACHACCGAACCCACTTGAATAATACATGCTGGAAC	1081
Db	2196	ATTTTACTGTCTCAGAGCATGTAGTATATATCTGAGCCCTCTTGATATCAAGACTGGAAG	2255
QY	1082	TACTATTTGATGCTTTTATAATCTTCTAATACAGTCTTAACTGGAAGCCAGAGGTTTG	1141
Db	2256	CAGGCTCAGATTTACTATATCCCGCAATACAGTACTTAATGTTAAACCTGAAATTTG	2315
QY	1142	GTTTCGATGTTCTTCTTAAATCGTTGGATGTATCCAGGTGGGGTGTTCGCCACCTCAGAAGAT	1201
Db	2316	GTTTCAGATGTTCTTCTTAAATCGCTGGACTCACCGCCTGGGTTCATTTGCCACCTCAGAAAT	2375
QY	1202	GGTACAGCAGAAATGTTTACACCTTAAAGCAACAGTTTACGTTCCAGAGATGCTTA	1261
Db	2376	GTCCGCTCTGAAATGGCACCCATGTCTAGAGCAACTGTGAAGGTTTCCATTTGATGATCA	2435

QY	2323	TGACCTTACGACGAGCCTCTCTCGCATCTGATATACGCTGGCTCTGACTTCATCTCTGGTCC	2382
Db	661	TGACCTTACGACGAGCCTCTCTCGCATCTGATATACGCTGGCTCTGACTTCATCTCTGGTCC	720
QY	2383	CATCTATATTTGAGCCTTGGGCTTAACCTCAGCTCGTCGCATCGGGTATCGAACCATCC	2442
Db	721	CATCTATATTTGAGCCTTGGGCTTAACCTCAGCTCGTCGCATCGGGTATCGAACCATCC	780
QY	2443	CGATTTGCCACGACACTGGAGGCTCTTCGACACTGCTTCGATGTGACAAATGACAAGG	2502
Db	781	CGATTTGCCACGACACTGGAGGCTCTTCGACACTGCTTCGATGTGACAAATGACAAGG	840
QY	2503	AACGAGCCCGAGATCGAGGCTTTGAGCCCAACGGGTTTAGCTTTGACGGAGCTGATGCA	2562
Db	841	AACGAGCCCGAGATCGAGGCTTTGAGCCCAACGGGTTTAGCTTTGACGGAGCTGATGCA	900
QY	2563	ACGGTGTGTACTACGGCTGAAACAGGCGGATCTCAG	2598
Db	901	ACGGTGTGTACTACGGCTGAAACAGGCGGATCTCAG	936
RESULT 7			
US-10-425-114-30909			
; Sequence 30909, Application US/10425114			
; Publication No. US2004003488A1			
; GENERAL INFORMATION:			
; APPLICANT: Liu, Jingdong			
; APPLICANT: Zhou, Yihua			
; APPLICANT: Kovalic, David K.			
; APPLICANT: Screen, Steven E			
; APPLICANT: Tabaska, Jack E			
; APPLICANT: Cao, Yongwei			
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With			
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement			
; FILE REFERENCE: 38-21(53313)B			
; CURRENT APPLICATION NUMBER: US/10/425,114			
; CURRENT FILING DATE: 2003-04-28			
; NUMBER OF SEQ ID NOS: 73128			
; SEQ ID NO 30909			
; LENGTH: 2561			
; TYPE: DNA			
; ORGANISM: Zea mays			
; FEATURE:			
; OTHER INFORMATION: Clone ID: UC-ZMFLB73098B08_FLI			
US-10-425-114-30909			
Query Match 31.8%; Score 826.4; DB 13; Length 2561;			
Best Local Similarity 66.4%; Pred. No. 3.9e-237;			
Matches 1411; Conservative 0; Mismatches 396; Indels 317; Gaps 3;			
QY	780	TTGACTCGGGTTTTTGTGACGGCCACACAGGAGTGAAGAAATATGACAAATGGA	839
Db	2	TTTGATCGGGTTTTTGTGATGGCCACCTGGGAATGCAAGAAATATGATACAAATGGA	61
QY	840	GGACATGATTTTCATGCTACCCCTTCCAAATAACATGACTGAGGAAGAGTATGGATGGAA	899
Db	62	AGACAGGATTTCCATGCTATCGTTCCGAATAACATATCGATGATATCTTTGGGTGGAA	121
QY	900	GAAGAACAAAGATCTATACAGGCTTCAACAGAGAGGAGGAAAGGAGGAGGCTATT	959
Db	122	GAAGAACATAGATCTTTTACAAGGCTTCAACAGAGAGAGAGGAAGGGAGGGCGCTGAA	181
QY	960	AAAGGAGGCTTGAGAGAAATGCAAAATGAAAGCTGAGATCAAGGAAAGACTATGAGA	1019
Db	182	AGATAAAGGCTGAGAGATCTGCAAAATGAAAGCTGAGATGAGAGAAAGACTATGAGA	241
QY	1020	ATGTTCTCGGTTTCTCAGAAACACATTTGTTACACCGAACCACTTGAATAATCATGCTGA	1079
Db	242	CGGTTTCTGCTTTCACAAAACATATTGTATATCTAGCCGCTCGAAGTACATGCAGGA	301
QY	1080	ACTACTATGTAGTGCTTTATAATCCCTTCTAATACAGTTCTTAAGTGAAGCCAGAGGTT	1139

QY 1140 TGGTTTCAGATGTCCTTTAAATCGTTGGATGATCCAGTGGGGTGTGGCCACCTCAGAAG 1199
DB |||||
DB 362 TGGTTTCAGAGGTTCTTTTAAACGGTTGGACTCATCCAGTGGTCCCTTACCACCCAGAAAG 421
QY 1200 ATGGTACAGCAGAAAATGGTTTCACACCTCAAAAAGCAACAGTTAGTTTCCACGAGATGCC 1259
DB |||||
DB 422 ATGGTAAAGGCTGAGAATGGTTTCACACTTACGAACAACAG---GGTTCCTTGGATGCA 477
QY 1260 TATATGATGGACTTCCTGTTTTCGAGAGTCAGAAAGTGGTAATTTATGATAACAGAAAT 1319
DB |||||
DB 478 TATATGATGGACTTCCTGTTCTCTCAGTC---AGAAAGTGGTAATATATGACAAATAGGAAT 534
QY 1320 GGGTTAGACTATCATATTCCTGTTTGGTCAATTCGAAAGAACCACTATGACAAAT 1379
DB |||||
DB 535 GGGATGGACTATCATATTCCTGTTCTGATCTGTTGCAAGGGAACCTCCAAATGACATAT 594
QY 1380 GTCCACATTTGCTTGGATGGCAACCAATCGCAAGGTTGAGGTCCTTGGTGAATTTGTC 1439
DB |||||
DB 595 GTACACATTCAGTGGAAATGGCTCTATCGCAAGGTCGGAGGCTTTGGTGAATTTGT 654
QY 1440 ACTAGTCTTTACGTCGCTGCAAGATTTAGACACAAATGTGGAGGTTATTTCTCCAAAG 1499
DB |||||
DB 655 ACAAGCCTTTTACGAGCTGTTCAAGATTTAGGCCATTAAGTTGAGGTTATTTCTGCCGAAA 714
QY 1500 TACGGTTGCTTCAATCTAAGCA----- 1521
DB |||||
DB 715 TATGATTTGTTAAACCTTTAAACAGTGAAGTTTGTCTACTGGTGTAAATGTCTGGTCT 774
QY 1522 ----- 1521
DB 775 TCTTTTCTTCCCTTTTATCTGTCCTCCTCACCTTTCTTTTCAATTTCCAAATTT 834
QY 1522 ----- 1521
DB 835 CAGCGTCTTTTTCACCTTCAAGATGTGAGTTCAATTTAGTTTAAAGCACATGAATTTA 894
QY 1522 ----- 1521
DB 895 TGGAGGAGAAATATCTTAATGTGTGCTCTTTTCAATTTAATCTGCAGTACCTTTTATG 954
QY 1522 ----- 1521
DB 955 TTATTTTGGAGAGTTTCATGTGTATGGATGATGACCAATGGTAGTTGGTGGATACCAA 1014
QY 1522 ----- 1521
DB 1015 TTTTCTTCAATATGTGGCGTCTTCGGTTGCAGGTGAAGGATTTACGCTACCAACAAG 1074
QY 1550 TTTTCTTGGGGTGGTTCTGAAATAAATGTGGCGTGGACTAGTCGAAGGCTTTGTGT 1609
DB |||||
DB 1075 TTTTACTTGGGTGGGCACAGATGATAAAGTATGGTTTGAAGGTTGAAGATCTCCCTGT 1134
QY 1610 TTACTTCTGGAACCTCAAAATGGGATGTTTGGATCGGATGATGATATGGCAGGACGA 1669
DB |||||
DB 1135 TTATTTCTTGGAAACCAAAATGGGATGTTTGGGTGGATGTCTACCGGAAGAATGA 1194
QY 1670 TGACCGCGATTTGGCTTCTTCTGCTGCTCTGCTCTGAGAGTTTCTCTCCAAAGTGGATC 1729
DB |||||
DB 1195 TGAGAGTAAATTTGGGTTCTTCTGCTCTGCTCTGAGTTTGTCTCCAAAGGATC 1254
QY 1730 TTTCTCGAATATAATACATTTGCCATGATTTGGTCAAGTGTCTCTGTTTGGCTGCTACAAA 1789
DB |||||
DB 1255 TTTCTCTGATATCATACATTTGTCATGTTGGTCAAGTGTCTCCGTTTGGCTGTGACAA 1314
QY 1790 GGAAACTACGGGAAGTCTAGCTTGGCAACGACGCGGTGGTATTCACCATCCAAATCT 1849
DB |||||
DB 1315 GGAACATTAATGCTTTTAAATGGGATCGGAAATGGTGGATTTGATTTACCATCCAAATCT 1374
QY 1850 TGAATTTGGAGCGCATCATATTTGGCAAGCAATGAGATATTTGTGATAAAGCAACACTGT 1909
DB |||||
DB 1375 TGAGTTTGGAGCGCATCATTTGGCAAGCAATGGCAATTTGTGACAAAGCTACAACTGT 1434

QY 1910 CTCTAATACATATTTCAAGGAAGTGTGAGTCTAGTTCATGTCCTCATGTTTCTCTCTTGGAA 1969
DB |||||
DB 1435 ATCCGATACATCTCGAAGGAAGTGGCGGACATGGAGCTATTTCACCTCACTACTATAA 1494
QY 1970 ATTCTATGGCAATTTCTAATGGAATGTATCCGGATATATATGGAATCCGTACAACTT 2029
DB |||||
DB 1495 ATTCCATGGAATTCGAAATGGAATGTATCTCGATATTTGGATATCATATATGCAAAAT 1554
QY 2030 TATCCCGTCCACTACACTTTGTGAAGATGTGTTGAAGGCAAGAGGCTGCTAAGAGGC 2089
DB |||||
DB 1555 TATTCGGTCAATTTATATCATCAGAAATGTTTGTGAGGCAAGAGTCTGCAAAAAGGC 1614
QY 2090 ACTCAGCAGAAAGTTTGGGTTTACGCAAAATCGATGTCCCCGTCTGAGAAATCGCTCG 2149
DB |||||
DB 1615 ATTCCAGCAGATCTTGGATTACAGCAAACTGATACCCCTGTTTGTGGAATCATCACTCG 1674
QY 2150 CCTGACAGCCCAAGAGGATCCACCTGATCAAGCATGCCGATTCACCGTACACTCGAAG 2209
DB |||||
DB 1675 TCTAACAGTTTCAAGAGGAAATCCACCTTATCAAAATGCAATGCAATGAGCTCTTGAACG 1734
QY 2210 GAACGGACAGTGTGTTTGTGTTTCAGCGCCGAGCTCTCGAATCCAAAGCTGATTTGT 2269
DB |||||
DB 1735 CAATGGACAGTGTGTTTACTGGGTTCTGACACAGATCTTCCGATACAAAGTGAATTTAC 1794
QY 2270 CAACCTGGCGAATACGCTCCACGGCGTAACCAATGGGCAAGTGAGGCTTTCTTTGAACCTA 2329
DB |||||
DB 1795 AAATTTGGCCAGTAAGCTGCAATGCTGTAATCATATGGCGGAGTGAAGCTATGCTTAAACCTA 1854
QY 2330 CGACAGGCTCTCTCGATCTGATATACGCTGGCTCTGACTTCAATCTGCTCCCATCTAT 2389
DB |||||
DB 1855 TGACGAGCACTGTCAATTTGATATATGCTGGCGAGACTTCATTTCTGTTCTTCAT 1914
QY 2390 ATTTGAGCTTTCGGCCCTAACTCAGCTCTCGCATGGGTATGGAACCATCCGAGTTGT 2449
DB |||||
DB 1915 CTTGAACTTTGTTGTTCTTAAACAGCTTTATGCTATGGCTATGATCCATCCAGTTGT 1974
QY 2450 CCGCAAGACTCGAGGCTCTTTCGACACTGTCTTCGATGTGCAACAATGACAAAGAACGAGC 2509
DB |||||
DB 1975 TCGGAAAACCTGGAGGCTGTACGACACCGTTTTTGTGTCACAATGATAAGGATCGGGC 2034
QY 2510 CCGAGATCGAGGCTTGGCCCAACGGGTTTAGCTTTGACGGAGCTGATAGCAACGGTGT 2569
DB |||||
DB 2035 TCAAGCAAGGCTCTCGAGCCAAATGGATTCAGTTTCGAAGAGCTGATAGCAGTGGTGT 2094
QY 2570 TGACTACGCTGTGAACAGGGCGAT 2593
DB |||||
DB 2095 GGATTTCTCTCGACAGAGCCAT 2118

RESULT 8

US-10-424-599-97896
; Sequence 97896, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 97896
; LENGTH: 2218
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59413C.1
US-10-424-599-97896

Query Match

27.9%; Score 724.4; DB 13; Length 2218;

Best Local Similarity 71.7%; Pred. No. 1.9e-206;
Matches 977; Conservative 0; Mismatches 381; Indels 4; Gaps 2;

QY 1240 TTTCAGTTCCACGAGATGCCATATATGATGACTTCGTTTTCGAGAGTCAGAAAGGTTG 1299
DB TTAAGGTTCCACATGGATGATATATGATGACTTCGTTTTCGAGAGTGAACATGGTG 72
QY 1300 GAATTTATGATTAACAGAAATGGGTAGACATATATATCTGTTTTCGAGTCAATTCGAA 1359
DB GAGTTTTTGTATACAAATTTGGAATGATAT-ACATACAGATTTTGGAAATTTGCAA 131
QY 1360 AGGAACACCTATGTCACATGTCACATGCTGTGAGATGGCACAAATCGCAAGGTTG 1419
DB 132 AGGAACACCTTTGATATATCATATGCTGTGAGATGGCCCAATTTGCAAAAGTTG 191
QY 1420 GAGGTTCTGGTGTATGTTCTACTAGTCTTTCAAGTGTGTCAGAGATTTTAGGACAAATG 1479
DB 192 GAGGCTTTGGTGAGTTGTTACTAGTCTATCCGGGCTGTTCAGGATTTAAATCACAATG 251
QY 1480 TGGAGTTATCTTCCAAAGTACGGTGTGCTGATCTTAAGCAATGTCAGAACTACAA 1539
DB 252 TGGACATCATCTTCCAAAGTATGACTGCTGTAACCTTAGCAATGTAAAGGACTTTGACC 311
QY 1540 TCCATCAGAGTTTCTTGGGGTGTCTGAAATAAATGTGCGGTGGACTAGTCGAAG 1599
DB 312 GTCATAGATTTTCGCTCGAGGGACTGAATAAAGTATGGCATGGAAAGTTGAAG 371
QY 1600 GCCTTTGTGTTACTTCTCGAACCCTCAAAATGGATGTTTGGAGTCGGATATGATATG 1659
DB 372 GCCTCTCTGCTACTTTTGGAGCCTCAAAATGGATCTTTCAGGTTGGCTGTATATG 431
QY 1660 ---GCAGGACGATGACCGCGATTTGGCTTCTGCTGCTGCTGCTAGAGTTCTCC 1716
DB 432 GTCGTGGGAATGATGGAGAGATTTGGTTTTTTTGTGTCGCGCTCTCGAGTTCTAC 491
QY 1717 TCCAAAGTGATCTTCTCCGAACATAATATGCCATGATTTGCTCAAGTCTCCTGTTG 1776
DB 492 TCCAAAGTGATTTTCATCTTGATATCATCATGCTGCAATGATGCTCAAGTCTCCGGTTG 551
QY 1777 CTTGGCTTACAAAGGAAATACGCGAAGTCTAGTTGGCAACGCAACGGGTGGTATPCA 1836
DB 552 CATGGCTATTAAAGACAACTATGCACATATGCTTTAGTAAAGCACGAGTTGCTTCA 611
QY 1837 CCATCCACATCTTGAATTTGGAGCGCATCATATTTGCAAGCAATCAGATATTTGATA 1896
DB 612 CAATTCATACTTGAATTTGGAGCCCATTCATTTGAAAGAGCTATGCGATATGCTGACA 671
QY 1897 AAGCAACAACTGCTCTAATACATATTTCAAAGGAAGTGTGAGTCTAGTGGCCATAGTTC 1956
DB 672 AAGCTACAACCTGCTCTCCACATATTTCAAGAGAGATTTGCTGTAATCTGTAATGCTC 731
QY 1957 CTCACTTTGGAAATTTCTATGGCAATTTCTAATGGAATTTGATCCGATATATGGAATCCGT 2016
DB 732 CTCACTTTCAAGTTCATGGTATATAAATGGAATTCGACCCAGATATATGGAACCCAT 791
QY 2017 ACAATGACAACTTTATCCCGGTCACACTTGTGAGAAATGTTGTTGAAGGCAAGAGG 2076
DB 792 ATATGATAAATTCATTTCCCGGTATCATCTCTTCAAGAAATGTTGTTGAAGGAAAGAG 851
QY 2077 CTGTAAGAGGGGCACTGACGAGAAAGTTTGGGTTTACAGCAATTCGATGTCCCGCTCGTAG 2136
DB 852 CTTTGAAGGAACCTTGCAACAAAGGCTTAGTTTAAAGAAAGCTGATCTTCTTTAGTG 911
QY 2137 GAATGCTCATCTGGCTGACAGCCCAAAAGGGGATTCACCTGATCAAGCATGCGAATTCACC 2196
DB 912 GAATTAATTAATCTGATGACTCATCAGAAAGGAATCCATCTCATCAACATGCGCATATGGC 971
QY 2197 GTACACTCGACGGAACGACAGATGTTTGTGTTGTTTGTGCTGAGCGCGGACTCTCGAATCC 2256
DB 972 GCACCCTAGAACGTTGGGACAGGTTGTACTTGTGTTTGTGCTGAGTCCAGATCTCGATACC 1031
QY 2257 AAGCTGATTTTGTCAACTGTCGGAATACGCTCCACGGCGTAAACCATGGGCAAGTGAGGC 2316

DB 1032 AAAATGATTTTGTGAATTTGGCCAAATGAATTCGATTCGCTCATCATGATCGTGTAGAC 1091
QY 2317 TTTCCTTGACCTTACGAGAGCGCTCTCTCGATCTGATATACGCTGGCTCTGATCTTCAATTC 2376
DB 1092 TTTCCTTGCAATGATGAGCCTCTTTCACATCTGATATATGCTGTGCTGATTTCAATTC 1151
QY 2377 TGGTCCCATCTATATTTGAGCTTGGGCTTACTCAGTCTGTCGCGCATGCGGTATGGAA 2436
DB 1152 TAGTTCCTTCAATCTTTTGGCCATGTTGACTCTCACTCACTCAAGCAATGAGATATGGTT 1211
QY 2437 CCATCCCGATTTGTCGCAAGACTTGGAGGCTCTTTCACACTGTCTTCGATGTGCAAAATG 2496
DB 1212 CAATACCTGTTGTTGCGAAAACCTGGAGGACTTTACGATACAGTATTCGAGCTTGACCAATG 1271
QY 2497 ACAGAAAGAGCCCGAGATCGAGGCTTGGAGCCCTTGGAGCCCAACGGGTTAGCTTTGACGGAGCTG 2556
DB 1272 ATAAGGATGAGCCCAAGCGCAAGGCTTTGAGCCAAATGATTTAGTTTTTGTATGGAGCTG 1331
QY 2557 ATAGCAACGCTGTTGACTAGCGCTGACAGAGGCGGATCTCAG 2598
DB 1332 ATACTGAGGCTTGTGATTTATGCTCTCATAGGCAATATCAG 1373

RESULT 9

US-10-425-114-4321

; Sequence 4321, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jindong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 4321

; LENGTH: 1181

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: 700379870_FLI

US-10-425-114-4321

Query Match 18.5%; Score 480.4; DB 13; Length 1181;
Best Local Similarity 76.9%; Pred. No. 4e-133;
Matches 586; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

QY 1832 ATTCAACATCCCAATCTTGAATTTGGAGCGCATCATATTGGCAAGCAATAGATATTG 1891
DB 1 ATTTACCATCCAACTCTTGAGTTTGGAGCGCATCACTTGGCAAGCAATGCAATG 60
QY 1892 TGAATAAGCAACATCTCTTAATACATATTCAAGAGAGTGTGAGTTCATGTCCTAT 1951
DB 61 TGACAAAGCTACAACTGTATCCGATACATCTCGAAGGAAGTGGCGGACATCGAGCTAT 120
QY 1952 AGTTCTCATCTTGGGAAATTTCTATGGCATTCATGAATGAAATTCGATCCGATATATGGGA 2011
DB 121 TGACCTTCACTACTATAAATTCATGGAATTCGAATGGAATTCCTGATATTTGGGA 180
QY 2012 TCGGTCAATGACAACTTTATCCCGTCCACTACACTTGTGAGAATGTGTTGAAAGCAA 2071
DB 181 TCCATATCTGACAAATTTATTCGGTCCATTATACATCAGAGAATGTTGTTGAGGCAA 240
QY 2072 GAGGCTGTAAAGGGCACTGACGAGAGATTTGGTTTACAGCAAAATCGATGTCCTCCGT 2131
DB 241 GAGTGTGCAAAAAGGCAATTCAGCAGATGCTTGGATTACAGCAAACTGATACCCCTGT 300
QY 2132 CGTAGGAATCGTCACTCGCTCGACGCCCAAGGGGATCCACCTGATCAAGCATGGAT 2191

301	DB	TGTTGGAATCATCACTCGTCTAAACAGTTTCAAGAGGGAATCCACTTATCAACATGCAAT	360
2192	QY	TCACCGTACACTCGAACGGAAACGACAGGTGGTTTTCGCTTTCAGCGCGGACACTCTCG	2251
361	DB	GCATCGAGCTCTTTGAACGCAATGACACAGGTGGTTTTCATCGGGTTCTGCACCATGCTCG	420
2252	QY	AATCCAGCTGATTTTGTCAACCTGCGGAATACGCTCCACGGGTAAACCATGGGCAAGT	2311
421	DB	CATTAAGAATGACTTTTACAAATTTGGCCAGTAAGCTGCATGGTGAATACCATGGCCGAGT	480
2312	QY	GAGGCTTTCTTCACCTACGACGAGCCTCTCTCGCATCTGATATACGCTGGCTCTGACTT	2371
481	DB	GAAGCTATGCTAAACCTATGACGAGCCACTGTCACTTTGATATATGCTGGCGCAGACTT	540
2372	QY	CATTCTGGTGCCATCTATATTTGAGCCCTTCGGGCTTAACCTAGCTGTCGCCATGGGTA	2431
541	DB	CAITCTGGTTCTTCCACTCTTCGAACTTTGTGGTCTAACACAGCTTATTGCTATGGCCTA	600
2432	QY	TGGNAACATCCGATTCGTCGCAAGACTGGAGGCTCTTCGACACTGCTTTTCGATGTGA	2491
601	DB	TGGATCATCCAGTTGTTCGAAAACTGGAGGCTGTACACACCGTTTTGATGTGCA	660
2492	QY	CAATGACAAAGAAACGAGCCCGAGATCAGGCGCTTGTAGCCCAACGGGTTTATGCTTTGACGG	2551
661	DB	CAATGATAAAGATCGGGCTCAAGCACAAAGTCTCGAGCCAAATGGATTTCAGTTTCGAAGG	720
2552	QY	AGCTGATAGCAACGGTGTGTGACTACGGCTGAAACAGGGCGAT	2593
721	DB	AGCTGATAGCAGTGGTGTGATTTATGCTTCGACAGAGCCAT	762

RESULT 10
US-10-341-961A-91
; Sequence 91, Application US/10341961A
; Publication No. US20040006787A1
; GENERAL INFORMATION:
; APPLICANT: Boyce Thompson Institute for Plant Research, Inc.
; APPLICANT: Crusta, Oswald
; APPLICANT: Swirsky, Peter
; APPLICANT: Mysore, Kiran
; APPLICANT: Folkerts, Otto
; APPLICANT: Martin, Gregory
; APPLICANT: Ekengren, Sophia
; TITLE OF INVENTION: PLANT DEFENSE-RELATED GENES REGULATED IN RESPONSE TO PLANT-PATHOGEN
; TITLE OF INVENTION: PLANT DEFENSE-RELATED GENES REGULATED IN RESPONSE TO PLANT-PATHOGEN
; FILE REFERENCE: BTI.67A2
; CURRENT APPLICATION NUMBER: US/10/341.961A
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: 60390249
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 60261029
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60348792
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-10-341-961A-91

	Query Match	12.2%	Score 315.8	DB 16	Length 585
	Best Local Similarity	71.4%	Ered: No. 9.4e-84		
	Matches 416	Conservative	0	Mismatches 167	Indels 0
	Gaps	0			
QY	1030	TTTCTCAGAAACACATCTTTTACACCGAACCACTTGAAATACATCGCTGGAACTACTATTG	1089		
Db	3	TGCTCTCAGAAGCATGTAGTATATATCTAGCCCTCTTGATATCCAAAGCTGGAGACAGCTCA	62		
QY	1090	ATGTGCTTTATAATCCCTTCTTAATACAGTTCTTAACCTGGAAGCCAGAGGTTGGTTTCGAT	1149		

Db	63	CAGTTTACTATATATCGGCGCAATACAGTACTTTAAATGGTAAACCTGAAATTTGGTTCAGAT	122
Qy	1150	GTTCCCTTAAATCGTGGATGTATCCAGGTGGGGTGTGCCACCTCAGAAGATGGTACAAG	1209
Db	123	GTTCAITTTAATCGCTGGACACACGGCTGGTCCATTGCCACCTCAGAAAATGTTGCCTG	182
Qy	1210	CAGAAAATGGTTTACACACCTAAAAACCAACAGTTTACGTTCCACGAGATGCCATATATATGG	1269
Db	183	CTGAAAATGSCACCCATGTCAAAGCAACTGTCAAGGTTCCATTGGATGCATATATATGG	242
Qy	1270	ACTTCGTTTTCTCGGAGTCAGAAGAAGTGGAAATTTATGATACAGAAATGGGTTAGACT	1329
Db	243	ATTTTGTAATTTCCGAGAGAGAAGATGGTGGTATTTTGTGACATAGAGCGGAATGGACT	302
Qy	1330	ATCATATTCCTGTTTTGGGTCAATTGCAAGGAACCACTATGTCACATTTGCCACATTC	1389
Db	303	ATCACATACCCGTGTTGGAGGAGTCGCTAAGAACCTCCGATGCATATTTGTCATATTG	362
Qy	1390	CTGTTGAGATGGCACCAATCGCAAGAGTTGGAGGTCGTGGTGATGGTTGTCACTAGTCTTT	1449
Db	363	CTGTGCAAAATGGCACCAATTTGCAAAAGTGGGAGGCCCTTGGTGATGTTGTTACTAGCCTTT	422
Qy	1450	CAGTGTGTTGCAAGATTTAGGACACAATGTGAGGTTATTCCTCCAAAGTACGGTTGCT	1509
Db	423	CCCGTGCTGTTCAGATTTAAACATAATGTGACATATCTTTACCTAAGATATGACTGTT	482
Qy	1510	TGAATCTTAAGCAATGTCAAGAATCTACAAATCCATCAGAGTTTTTCTTGGGGTGGTTCTG	1569
Db	483	TGAAGATGAATATGTGAAGGACTTTCGGTTTCACAAAAGCTACTTTTGGGTGGGACCTG	542
Qy	1570	AAATAAATGTGGCGTGGACTAGTCGAAGCCCTTTGTGTTTA	1612
Db	543	AAATAAAGATGTTTTGGAAGGTGGAAGGACTCTCGGTCTA	585

```

RESULT 11
US-09-739-438-3
; Sequence 3, Application US/09739438
; Patent No. US2002029394A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Beckles, Diane M.
; APPLICANT: Thorpe, Cathy
; TITLE OF INVENTION: Homologs of Starch Synthase DUI
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/739,438
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/171514
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (312)
; NAME/KEY: unsure
; LOCATION: (408)
; NAME/KEY: unsure
; LOCATION: (548)
US-09-739-438-3

```

	Query Match	11.2%	Score 290.6;	DB 9;	Length 548;
	Best Local Similarity	79.9%;	Pred. No. 3.5e-76;		
	Matches 341;	Conservative	0;	Mismatches 86;	Indels 0; Gaps 0;
QY	1661	CAGGACAGATACCGCGCATTTGGCTTCTTCTTCGTCTCTCTAGAGTTCTTCCTCCA	1720		
Db	3	CAGCAATCAGCAGAGTAGATATTTGGCTTCTTCTTGGCAATTCGCTCTAGAGTTCTTCGCGCCA	62		

Db 122 TAAAGCTTTGTTTAACTATGATGAGCGCACTATCTCAATTGATTGCTGGTCCGCACT 181
Qy 2371 TCATTCTGGTCCCACTATATTTGAGCCTTGGCGCCTAACTCAGCTCGTCCCAATGCGGT 2430
Db 182 TCATCCCTTGTTCCCTCCATGTTTGAACCTTGTTGTTTAAACCCAGCTTACTGCTATGCGTT 241
Qy 2431 ATGGAACCATCCCGATTGTCGGAAGACTGAGGGCTCTTCGACACTGTCTTCGATGCG 2490
Db 242 ATGGATCTATCCCAATAGTTCCGAAAACGTGAGGCCCTTATGACACCGCTTTTTCACGTCG 301
Qy 2491 ACAATGACAAGGACGAGCCGAGATCGAGCCTTGAGCCCAACGGGTTTAGCTT-TGAC 2549
Db 302 ACGATGATGAGATCGAGCTCGACACAGGCTTTCGACCAACGGGTTCAATTTCCGAA 361
Qy 2550 GGAGCTGATGACAA-CGGTGTGACTAGCGCTCGAACAGGGCGATCTC 2596
Db 362 GGAGCTGACANCAACGGGCTGTGGATTACCCCTTTGACAAAGCNATCAC 409

RESULT 14
US-10-424-599-84418
; Sequence 84418, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kowalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 84418
; LENGTH: 464
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MPT3847_47245C.1
US-10-424-599-84418

Query Match 7.2%; Score 186.2; DB 13; Length 464;
Best Local Similarity 62.6%; Pred. No. 9e-45;
Matches 290; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

Qy 300 AATGATTTCTGATACAAATAGAAAGCAACCATGATGAAATTTTATTTGAGATTTCTTG 359
Db 2 AAAGACTTCTGCATACCCGTTTGATGGAGGATGGATGCAATTAGCAATTTGAAGATTTCTTG 61

Qy 360 GCTGAGAAAGCAACGAGAACTTGAGAACCTTGCAATGAGGAGCTGAAAGGAGGAGA 419
Db 62 CTTGAGGAGAAACGTPAAGAAATTGAAAGAACTTGCTGGGCCAAGCTGAAAGGGAAGA 121

Qy 420 CAAACTGATGACAGCGGCGAATGAGGAGAAAGAGGCGCGAGATAAAGCTGACAGGGTA 479
Db 122 CAACTGAGAGCAAGGCGAATGAGGAGAGAGAGAGCTGCAAGGAGAGAGAGAGGCA 181

Qy 480 CAAAGCAAGGTTGAGGTAGAGACGAGAAAGAAATAAATTGTGCAATGTATTTGGTTTAGCC 539
Db 182 CGGGCGAAGGCGGAGGTTGGAAGATCGGAGAAACATTTGCCACAATTTGTGAAAAATGCT 241

Qy 540 AGAGCTCCTGTTGATAATTTATGTATACATTGAGCCCATCAGCTGGACAGAGGCTACT 599
Db 242 GTAAAGTCCATTGATAATTTGGTATATTTGAACCTAGTGAATTCAAAGGCAATGAAATTG 301

Qy 600 GTCAGATTGATTAATAACATAAATCAAGACCTCTAGTTTCACAGTACTGAGATATGGATG 659
Db 302 ATCAGATTATATTAACAGAGCTCAGTCTCTTGTGCAATGCTTAATGAATATGGATT 361

Qy 660 CATGTGGCTATAACAAATTTGATGAGCTCTCTTTTGTGAAAGGCTTTTTCATCAT 719
Db 362 CATGGGGGCACAATAAATTTGGAAGTATGGATTATCAATGTTGAAAGGCTTGTCAAGTCT 421

Qy 720 CATGACAAAGATTGATTTGGTGGTTCGATTTGCAGATGTTTGTGTCG 762
Db 422 GTTCTAAAAAGAGGTGAATGGTGTATGCTGATGTTGTTGTAC 464

RESULT 15

US-09-294-093B-3346
; Sequence 3346, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 3346
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700379870H1
; NAME/KEY: unsure
; LOCATION: 2, 56, 78, 121, 125, 155, 187-188, 197, 270
; OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-3346

Query Match 7.1%; Score 183.8; DB 9; Length 297;
Best Local Similarity 77.1%; Pred. No. 3.3e-44;
Matches 229; Conservative 0; Mismatches 67; Indels 1; Gaps 1;

Qy 1832 ATTCACCATCCACAATCTTGAATTTGGCGCATCATATTGGCAAGCAATGAGATATTG 1891
Db 1 ANTACCATCCACAATCTTGAATTTGGCGCATCATATTGGCAAGCAATGAGCAATTTG 60

Qy 1892 TGATAAAGCAACAACCTGTCTTAATACATATTCAAAGGAAGTGCAGTCAATGGTCCAT 1951
Db 61 TGACAAAGCTACACTGATCCGATACATCTCGAAGAACTGGCGGACATGGAGCTAT 120

Qy 1952 AGTTCTCATCTTGGGAAATTTCTATGGCATTTCTCAATGGAATTTGATCCGGATATATGGGA 2011
Db 121 NGCANTCACTACTATATAAATTCATGGAATTCGANATGGAATTTGATCCTGATATTTGGGA 180

Qy 2012 TCCGTACAAATGACAACTTTATCCCGTCCACTACACTGTGTGAGAAATGTTGTTGAAGGCAA 2071
Db 181 TCCATANNCTGACAAANTTATTCGGTCCATATATACATCAGAGAAATGTTGTTGAGGGCAA 240

Qy 2072 GAGGCTGCTAAGAGGCGACTGCGACAGAACT-TTGGTTTACAGCAAAATGATGTC 2127
Db 241 GAGTGTGCAAAAAGGCAATTCGACAGAGANTTACTGGATGACACGCAAACTGATACCC 297

Search completed: June 20, 2004, 13:20:02
Job time : 1501 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 20, 2004, 05:01:30 ; Search time 9811 Seconds
(without alignments)
7907.649 Million cell updates/sec

Title: US-10-634-262-1_COPY_2425_5022

Perfect score: 2598

Sequence: 1 agtbtgtgaaaaattat.....gtgaacaggcgatctcag 2598

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hcc:*

9: gb_est1:*

10: gb_est2:*

11: gb_hcc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_pbg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2468.2	95.0	6030	11	AY110586 Zea mays
2	771.4	29.7	971	14	CD437215
3	746.4	28.7	773	14	CA404552
4	731.6	28.2	751	14	CD445384

5	683.6	26.3	705	14	CD442124
6	577.6	26.1	692	14	CD434207
7	523.8	20.2	579	14	CA195121
c	519.8	20.0	535	14	CF051954
8	517.4	19.9	571	14	CD433067
c	517.4	19.9	831	12	BG319783
10	488.4	18.8	1014	14	CK247929
11	488.4	18.1	638	28	BZ970127
12	470.6	17.8	1042	14	CK207070
13	463.6	17.8	791	14	CD436069
c	461.8	17.6	466	14	CF038283
15	459	17.6	610	9	AW065975
16	456.6	17.6	695	14	CA498218
17	456.2	17.6	1024	14	CK206780
18	446.4	17.2	1024	14	BZ970123
19	439.4	16.9	662	28	BZ970123
20	438.8	16.9	646	13	BZ970115
c	436.4	16.8	782	10	AW448009
22	436.4	16.8	782	13	BQ605700
23	434.6	16.7	651	9	AV835062
24	431.4	16.6	441	14	CF647322
25	424.6	16.3	709	12	BG416819
26	418.8	16.1	804	11	AY110971
27	416.6	16.0	882	12	BI406367
28	414.2	15.9	602	12	BI075226
29	412.2	15.9	622	12	BJ479394
c	398.8	15.4	627	14	CD974691
30	398.8	15.4	805	14	CF436116
31	389.4	15.0	805	14	CF436116
32	378.4	14.6	827	14	CA764813
c	376	14.5	822	29	CG195829
33	375.2	14.4	556	13	BU970246
34	373.6	14.4	560	13	BU972071
35	369.4	14.2	627	12	BJ478159
36	369.4	14.2	627	12	BJ478159
37	363	14.0	548	13	CA096498
38	360.4	13.9	536	14	CD891997
39	359	13.8	680	12	BG591409
40	354.2	13.6	687	14	CA840457
41	352.4	13.6	613	14	CF588535
42	347	13.4	690	14	CF436584
43	340.8	13.1	545	12	BJ271418
44	326.8	12.6	555	9	AU101290
45	326.6	12.6	531	14	CD425532

ALIGNMENTS

RESULT 1	AY110586	AY110586	Zea mays	6030 bp	mRNA	linear	HTC 17-OCT-2002
LOCUS	AY110586	AY110586	Zea mays	6030 bp	mRNA	linear	HTC 17-OCT-2002
DEFINITION	AY110586	AY110586	Zea mays	6030 bp	mRNA	linear	HTC 17-OCT-2002
ACCESSION	AY110586	AY110586	Zea mays	6030 bp	mRNA	linear	HTC 17-OCT-2002
VERSION	AY110586.1	AY110586.1	Zea mays	6030 bp	mRNA	linear	HTC 17-OCT-2002
KEYWORDS	HTC	HTC	Zea mays	6030 bp	mRNA	linear	HTC 17-OCT-2002
SOURCE	HTC	HTC	Zea mays	6030 bp	mRNA	linear	HTC 17-OCT-2002
ORGANISM	HTC	HTC	Zea mays	6030 bp	mRNA	linear	HTC 17-OCT-2002
REFERENCE	HTC	HTC	Zea mays	6030 bp	mRNA	linear	HTC 17-OCT-2002
AUTHORS	HTC	HTC	Zea mays	6030 bp	mRNA	linear	HTC 17-OCT-2002
TITLE	HTC	HTC	Zea mays	6030 bp	mRNA	linear	HTC 17-OCT-2002
JOURNAL	HTC	HTC	Zea mays	6030 bp	mRNA	linear	HTC 17-OCT-2002
REFERENCE	HTC	HTC	Zea mays	6030 bp	mRNA	linear	HTC 17-OCT-2002
AUTHORS	HTC	HTC	Zea mays	6030 bp	mRNA	linear	HTC 17-OCT-2002
TITLE	HTC	HTC	Zea mays	6030 bp	mRNA	linear	HTC 17-OCT-2002
JOURNAL	HTC	HTC	Zea mays	6030 bp	mRNA	linear	HTC 17-OCT-2002

AY110586 Zea mays CL1800_1 mRNA sequence.
AY110586.1 GI:21214995
HTC.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 6030)
Hayney, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
Unpublished (2002)
2 (bases 1 to 6030)
Coe, E.H.
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of Missouri-Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the

maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB:

www.zmdb.iastate.edu.

Location/Qualifiers

1. .6030

/organism="Zea mays"

/mol_type="mRNA"

/db_xref="MaizeDB:630603"

/db_xref="taxon:4577"

/clone_lib="Maize Mapping Project/DuPont Cornsensus

Library"

/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match 95.0%; Score 2468.2; DB 11; Length 6030;

Best Local Similarity 95.1%; Pred. No. 0;

Matches 2470; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

```
QY 1 AGCTTGTGAAAAAATTATTCCTGGGAAACAAGTTGTTTACTTATCCAGATGTAATGA 60
DB 2425 AGCTTGTCTGNNNNNNNTATTTCCTGGGAAACAAGTTGTTTACTTATCCAGATGTAATGA 2484
QY 61 AAGCTGATTCACAAATGATCTCTATTTCATCGTGATCTATCAGCTGTGGCCAAATGAGC 120
DB 2485 AAGCTGATTCACAAATGATCTCTATTTCATCGTGATCTATCAGCTGTGGCCAAATGAGC 2544
QY 121 CTGATGTACTTATCAAGAGGACATTCATCGGTGGAGTGGAGATTTTTCAGTGAATAAT 180
DB 2545 CTGATGTACTTATCAAGAGGACATTCATCGGTGGAGTGGAGATTTTTCAGTGAATAAT 2604
QY 181 TGCACAGAGCGAGCTGGCAGGAGCTGGTGGTCTGCAAACTATACATTCCTAAGCAGG 240
DB 2605 TGCACAGAGCGAGCTGGCAGGAGCTGGTGGTCTGCAAACTATACATTCCTAAGCAGG 2664
QY 241 CATACAGAAATGGATTTGTGTTTTTAAACGACACACCGGTATATGAAATAATAACAATA 300
DB 2665 CATACAGAAATGGATTTGTGNNNNNNAAACGACACACNNNNNNNNNNNNNNNNNNNN 2724
QY 301 ATGATTTTCGTGATACAAATAGAAAGCCATGGATGAAATTTATTTGAGGATTTCTTGG 360
DB 2725 NNNNNNNCGTGATACAAATAGAAAGCCATGGATGAAATTTATTTGAGGATTTCTTGG 2784
QY 361 CTGAGAAAGACACGAGAACTTGAGAACCTTGCAAAATGAGAAAGCTGAAAGGAGGAGAC 420
DB 2785 CTGAGAAAGACACGAGAACTTGAGAACCTTGCAAAATGAGAAAGCTGAAAGGAGGAGAC 2844
QY 421 AAACTGATGAGCAGCGGCGATGGAGGAGAAAGAGGCGCGAGATAAAGCTGACAGGGTAC 480
DB 2845 AAACTGATGAGCAGCGGCGATGGAGGAGAAAGAGGCGCGAGATAAAGCTGACAGGGTAC 2904
QY 481 AAGCCAGGTTGAGGTAGAGACGAGAAAGATAAATTTGCAATGTATGGTTTGGTTAGCCA 540
DB 2905 AAGCCAGGTTGAGGTAGAGACGAGAAAGATAAATTTGCAATGTATGGTTTGGTTAGCCA 2964
QY 541 GAGCTCCGTTGATTAATTTATGTTGATATGAGCCCATCAGCACTGGACAAGAGGCTACTG 600
DB 2965 GAGCTCCGTTGATTAATTTATGTTGATATGAGCCCATCAGCACTGGACAAGAGGCTACTG 3024
QY 601 TCAGATTTGATTAATAACATAAATCAAGACCTCTAGTTTCACAGTACTGAGATATGGATGC 660
DB 3025 TCAGATTTGATTAATAACATAAATCAAGACCTCTAGTTTCACAGTACTGAGATATGGATGC 3084
QY 661 ATGTGGCTATAAATAATGGATGATGAGACTCTTTTGGTGAAGGCTTGTTCATCATC 720
DB 3085 ATGTGGCTATAAATAATGGATGATGAGACTCTTTTGGTGAAGGCTTGTTCATCATC 3144
QY 721 ATGACAAAGATTTGATTTGGTGGTTGAGATGTTGCTGCTGAAAGAACATATGAT 780
```

```
DB 3145 ATGACAAAGATTTGATTTGGTGGTTTGCAGATGTTGTCGTGCTGAAAGAACATATGTAT 3204
QY 781 TGGACTGGGTTTCTGCTGACCGGCCACACGAGGAGTGCAGAAATTTATGACAAATGTGAG 840
DB 3205 TGGACTGGGNNNNNNCTGACGGGCCACACGAGGAGTGCAGAAATTTATGACAAATGTGAG 3264
QY 841 GACATGATTTTCATGCTACCTTCCAAATTAACATGACATGAGGAGAGTATTCGATGGAG 900
DB 3265 GACATGATTTTCATGCTACCTTCCAAATTAACATGACATGAGGAGAGTATTCGATGGAG 3324
QY 901 AAGAAACAAAGGATCTATACAAAGGCTTCAACAGAGAGGAGGAGGAGGAGGCTATTA 960
DB 3325 AAGAAACAAAGGATCTATACAGGCGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNATTA 3384
QY 961 AAGGAGGCTGAGAGAAATGCAAAAATGAAGCTGAGATGAGGAGAAAGACTATGAGNA 1020
DB 3385 AAGGAGGCTGAGAGAAATGCGNNNNNTGAAAGCTGAGATGAGGAGAAAGACTATGAGAA 3444
QY 1021 TGTTCCTGGTTCTCAGAAACACATTTTACACGAAACCACTTGAAATACATGCTGGA 1080
DB 3445 TGTTCCTGGTTCTCAGAAACACATTTTACACGAAACCACTTGAAATACATGCTGGA 3504
QY 1081 CTACTATTGATGCTGTTTATAATCCTTCTAATACAGTTCTAACTGSAAGCCAGAGTTT 1140
DB 3505 CTACTATTGATGCTGTTTATAATCCTTCTAATACAGTTCTAACTGSAAGCCAGAGTTT 3564
QY 1141 GGTTCGATGTTCTTAAATCGTTGGATGATATCCAGGTGGGTGTTGCCACCTCAGAA 1200
DB 3565 GGTTCGATGTTCTTAAATCGTTGGATGATATCCAGGTGGGTGTTGCCACCTCAGAA 3624
QY 1201 TGGTCAACAGCAAAATGTTTACACCTAAAGCAACAGTTTACGTTCCACGAGATGCT 1260
DB 3625 TGGTCAACAGCAAAATGTTTACACCTAAAGCAACAGTTTACGTTCCACGAGATGCT 3684
QY 1261 ATATGATGACATTCGTTTCTCGGAGTCAGAGAGGTGGAATTTATGATAACAGAAATG 1320
DB 3685 ATATGATGACATTCGTTTCTCGGAGTCAGAGAGGTGGAATTTATGATAACAGAAATG 3744
QY 1321 GGTTAGCATATCATATTCCTGTTTTTGGGTCAATTCGAAAGCAACCACTATGACATG 1380
DB 3745 GGTTAGCATATCATATTCCTGNNNNNGGGTCAATTCGAAAGCAACCACTATGACATG 3804
QY 1381 TCCACATTTGCTGTTGAGATGGCACCAATCGCAAAGTTGGAGGTCTTGGTGTGTTGTCA 1440
DB 3805 TCCACATTTGCTGTTGAGATGGCACCAATCGCAAAGTTGGAGGTCTTGGTGTGTTGTCA 3864
QY 1441 CTAGTCTTTTCACTGCTGTGCAAGATTTAGGACACAATGTGGAGGTATTTCTTCCAAAGT 1500
DB 3865 CTAGTCTTTTCACTGCTGTGCAAGATTTAGGACACAATGTGGAGGTATTTCTTCCAAAGT 3924
QY 1501 ACGTTGCTTTGATCTTAAGCAATGTCAAGAAATCTCAAAATCCATCAGAGTTTTTCTTGG 1560
DB 3925 ACGTTGCTTTGATCTTAAGCAATGTCAAGAAATCTCAAAATCCATCAGAGTTTTTCTTGG 3984
QY 1561 GTGGTTCTGAAATAAATGTTGGGCTGGAGTCTAGTCGAAAGGCTTTTGTGTTTACTCTG 1620
DB 3985 NNNNNNNNNNTAAATGTTGGGCTGGAGTCTAGTCGAAAGGCTTTTGTGTTTACTCTG 4044
QY 1621 AACCTCAAAATGGGATGTTGGAGTCGGATATGATATGCGCAGGAGCATGACCGCGCAT 1680
DB 4045 AACCTCAAAATGGGATGTTGGAGTCGGATATGATATGCGCAGGAGCATGACCGCGCAT 4104
QY 1681 TTGGCTTTCTTCTGCTGTTCTGCTCTAGAGTTTCTCTCCAAAGTGGATCTTCTCCGAACA 1740
DB 4105 TTGGCTTTCTTCTGCTGTTCTGCTCTAGAGTTTCTCTCCAAAGTGGATCTTCTCCGAACA 4164
QY 1741 TAATACATTCGCATGATGTTGCTCAAGTCTCTGTTGCTTGGCTACACAAGAAATACG 1800
DB 4165 TAATACATTCGCATGATGTTGCTCAAGTCTCTGTTGCTTGGCTACACAAGAAATACG 4224
QY 1801 CGAAGTCTAGCTTGGCAAAACGACGGGTGGTATTCACCATCCCAATCTTGAATTTGGAG 1860
DB 4225 CGAAGTCTAGCTTGGCAAAACGACGGGTGGTATTCACCATCCCAATCTTGAATTTGGAG 4284
```


Wakeman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jla1@wakeman.rutgers.edu
Seg primer: T7.

FEATURES	SOURCE
1. <i>General</i>	
2. <i>Specific</i>	
3. <i>Other</i>	
4. <i>Other</i>	
5. <i>Other</i>	
6. <i>Other</i>	
7. <i>Other</i>	
8. <i>Other</i>	
9. <i>Other</i>	
10. <i>Other</i>	
11. <i>Other</i>	
12. <i>Other</i>	
13. <i>Other</i>	
14. <i>Other</i>	
15. <i>Other</i>	
16. <i>Other</i>	
17. <i>Other</i>	
18. <i>Other</i>	
19. <i>Other</i>	
20. <i>Other</i>	
21. <i>Other</i>	
22. <i>Other</i>	
23. <i>Other</i>	
24. <i>Other</i>	
25. <i>Other</i>	
26. <i>Other</i>	
27. <i>Other</i>	
28. <i>Other</i>	
29. <i>Other</i>	
30. <i>Other</i>	
31. <i>Other</i>	
32. <i>Other</i>	
33. <i>Other</i>	
34. <i>Other</i>	
35. <i>Other</i>	
36. <i>Other</i>	
37. <i>Other</i>	
38. <i>Other</i>	
39. <i>Other</i>	
40. <i>Other</i>	
41. <i>Other</i>	
42. <i>Other</i>	
43. <i>Other</i>	
44. <i>Other</i>	
45. <i>Other</i>	
46. <i>Other</i>	
47. <i>Other</i>	
48. <i>Other</i>	
49. <i>Other</i>	
50. <i>Other</i>	
51. <i>Other</i>	
52. <i>Other</i>	
53. <i>Other</i>	
54. <i>Other</i>	
55. <i>Other</i>	
56. <i>Other</i>	
57. <i>Other</i>	
58. <i>Other</i>	
59. <i>Other</i>	
60. <i>Other</i>	
61. <i>Other</i>	
62. <i>Other</i>	
63. <i>Other</i>	
64. <i>Other</i>	
65. <i>Other</i>	
66. <i>Other</i>	
67. <i>Other</i>	
68. <i>Other</i>	
69. <i>Other</i>	
70. <i>Other</i>	
71. <i>Other</i>	
72. <i>Other</i>	
73. <i>Other</i>	
74. <i>Other</i>	
75. <i>Other</i>	
76. <i>Other</i>	
77. <i>Other</i>	
78. <i>Other</i>	
79. <i>Other</i>	
80. <i>Other</i>	
81. <i>Other</i>	
82. <i>Other</i>	
83. <i>Other</i>	
84. <i>Other</i>	
85. <i>Other</i>	
86. <i>Other</i>	
87. <i>Other</i>	
88. <i>Other</i>	
89. <i>Other</i>	
90. <i>Other</i>	
91. <i>Other</i>	
92. <i>Other</i>	
93. <i>Other</i>	
94. <i>Other</i>	
95. <i>Other</i>	
96. <i>Other</i>	
97. <i>Other</i>	
98. <i>Other</i>	
99. <i>Other</i>	
100. <i>Other</i>	

ORIGIN

Query Match 29.7%; Score 771.4; DB 14; Length 971;
Best Local Similarity 99.2%; Pred. No. 1e-189;
Matches 775: Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY		1818	AAGCACGGGTGTTATTCACCATCCCAAACTCTTGAATTGGACGCATCATATTGGCAA	1877
Dd		5	AATGCACGGGTGTTATTCACCATCCCAAACTCTTGAATTGGACGCATCATATTGGCAA	64
QY		1878	GCAATGAGATATTGTGATAAAGCAAACAATGCTCTTAATACATATTCAAAAGGAAGTGCA	1937
Dd		65	GCAATGAGATATTGTGATAAAGCACAAACTGTCTTAATACATATTCAAAAGGAAGTGCA	124
QY		1938	GGTCATGGTGCCTAGTTCCTCATCTTTGGGAAATTTCTATGGCATTCCTCAATGGAAATTGAT	1997
Dd		125	GGTCATGGTGCCTAGTTCCTCATCTTTGGGAAATTTCTATGGCATTCCTCAATGGAAATTGAT	184
QY		1998	CCGGATATATGGGATCCGTTCAATATGACAACTTTATCCCGTCCAATACATTTGTGAGAAT	2057
Dd		185	CCGGATATATGGGATCCGTTCAATATGACAACTTTATCCCGTCCAATACATTTGTGAGAAT	244
QY		2058	GTGGTTGAAGCACAAGAGGGCTGTCTAAGAGGGCACTGCAGCAGAGAGTTGGTTACAGCAA	2117
Dd		245	GTGGTTGAAGCACAAGAGGGCTGTCTAAGAGGGCACTGCAGCAGAGAGTTGGTTACAGCAA	304
QY		2118	ATCGATGTCGCCGTCTAGGAATCGTCACTCGCTTGACAGCCCCAAAAAGGGATCCACCTG	2177
Dd		305	ATTGATGTCCCCTGCTGAGGAATCGTCACTCGCTTGACAGCCCCAAAAAGGGATCCACCTG	364
QY		2178	ATCAAGCATGCGATTCACCGTACACTCGAACCGAACCGCAGAGTGGTTTCTGTTGGTTCA	223
Dd		365	ATCAAGCATGCGATTCACCGTACACTCGAACCGAACCGCAGAGTGGTTTCTGTTGGTTCA	424
QY		2238	GGCCGGACTCTCGAATCCAAAGCTGATTTGTTCAACCTGGCGGAATACGCTCCACGGCGTA	2297
Dd		425	GGCCGGACTCTCGAATCCAAAGCTGATTTGTTCAACCTGGCGGAATACGCTCCACGGCGTA	484
QY		2298	AACCATGGGCAAGTCAGGCTTTCCTTGACCTACGACGAGCCTCTTCGCATCTGATATAC	2357
Dd		485	AACCATGGGCAAGTCAGGCTTTCCTTGACCTACGACGAGCCTCTTCGCATCTGATATAC	544
QY		2358	GTGGCTCTGACTTCATTTCTGGTCCCATCTATATTGAGCCTTGGCGCTTAACCTCAGCTC	2411
Dd		545	GCTGGCTCTGACTTCATTTCTGGTCCCATCTATATTGAGCCTTGGCGCTTAACCTCAGCTC	604
QY		2418	GTCCGCATCGGTATGGAAACCATCCCGATTGTCGCAAGACTGGAGGGCTCTTCGCACACT	2477
Dd		605	GTCCGCATCGGTATGGGAACCATCCCGATTGTCGCAAGACTGGAGGGCTCTTCGCACACT	664
QY		2478	GTCTTCGATGTGGCAAAATGACAAGGAAACGAGCCCGAGATCGAGGCCCTTAGGCCAACGGG	2537
Dd		665	GTCTTCGATGTGGCAAAATGACAAGGAAACGAGCCCGAGATCGAGGCCCTTAGGCCAACGGG	724
QY		2538	TTTAGCTTTGACGGAGCTGATAGCAACGGTGTGTGACTACGCGCTGAACAGGCGGATCTCA	2597
Dd		725	TTTAGCTTTGACGGAGCTGATAGCAACGGTGTGTGACTACGCGCTGAACAGGCGGATCTCA	784

1861	CGCATCATATTGGCAAGCAATGAGATATTGTGATAAAGCAACACTGTCCTCTAATACAT	1920
QY		
4285	CGCATCATATTGGCAAGCAATGAGATATTGTGATAAAGCAACAACTGTCTCTAATACAT	4344
DB		
1921	ATTCAAAGGAAGTGCAGGTTCATGGTGCCATAGTTCTTCATCTTCGGGAAATTCATATGGCA	1980
QY		
4345	ATTCAAAGGAAGTGCAGGTTCATGGTGCCATAGTTCTTCATCTTCGGGAAATTCATATGGCA	4404
DB		
1981	TTCTCAATGGAAATTGATCCGGATATATGGGATCCGTFACAATGACAACTTTTATCCGGTCC	2040
QY		
4405	TTCTCAATGGAAATTGATCCGGATATATGGGATCCGTFACAATGACAACTTTTATCCGGTCC	4464
DB		
2041	ACTACATTTGTGAGAAATGTGGTTGAAGGCAGAGGGCTGCTAAGAGGGCACTGCAGACAGA	2100
QY		
4465	ACTACATTTGTGAGAAATGTGGTTGAAGGCAGAGGGCTGCTAAGAGGGCACTGCAGACAGA	4524
DB		
2101	AGTTTGGGTTTACAGCAAAATCGATGTCCCGTCTGTAGGAATCGTCACTCCGCTCGACAGCC	2160
QY		
4525	AGTTTGGGTTTACAGCAAAATCGATGTCCCGTCTGTAGGAATCGTCACTCCGCTCGACAGCC	4584
DB		
2161	AAAAGGGGATCCACCTGATCAAGCATGCGAATCACCGTACACTCGAAACGGAACGACAGG	2220
QY		
4585	AAAAGGGGATCCACCTGATCAAGCATGCGAATCACCGTACACTCGAAACGGAACGACAGG	4644
DB		
2221	TGTTTTGCTTGTGTTACAGCCGGCACTCTCGAATCCAGCTGATTTTGTTCACCTGGCGA	2280
QY		
4645	TGTTTTGCTTGTGTTACAGCCGGCACTCTCGAATCCAGCTGATTTTGTTCACCTGGCGA	4704
DB		
2281	ATACGCTCCACGGGTAAACCATGGGCAAGTAGGGCTTCTCTTGACCTACGACGAGCCTC	2340
QY		
4705	ATACGCTCCACGGGTAAACCATGGGCAAGTAGGGCTTCTCTTGACCTACGACGAGCCTC	4764
DB		
2341	TCTCGCATCTGATATACGCTGGCTCTGACTTCAATTCGTGGTCCCATCTATATTTGAGCCTT	2400
QY		
4765	TCTCGCATCTGATATACGCTGGCTCTGACTTCAATTCGTGGTCCCATCTATATTTGAGCCTT	4824
DB		
2401	CGCGCTTAACCTCAGCTCGTGCCCATGCGGTTATGGAACCATCCGATGTGTCGCAAGACTG	2460
QY		
4825	CGCGCTTAACCTCAGCTCGTGCCCATGCGGTTATGGAACCATCCGATGTGTCGCAAGACTG	4884
DB		
2461	GAGGGCTCTTCGACACTGTCTTCGATGTGGCAATATGACAAAGGAACGAGCCGAGATCGAG	2520
QY		
4885	GAGGGCTCTTCGACACTGTCTTCGATGTGGCAATATGACAAAGGAACGAGCCGAGATCGAG	4944
DB		
2521	GCCTTGAGCCCAAACGGGTTTACGCTTTGACGGGAGCTGATAGCAACGGTGTGTGACTACGCGC	2580
QY		
4945	GCCTTGAGCCCAAACGGGTTTACGCTTTGACGGGAGCTGATAGCAACGGTGTGTGACTACGCGC	5004
DB		
2581	TGAACAGGGCGATCTCAG	2598
QY		
5005	TGAACAGGGCGATCTCAG	5022
DB		

RESULT 2	CD437215	971 bp	mRNA	linear	EST 03-JUN-2003
LOCUS	EL01N0370A09.g	Endosperm_3	Zea mays	cdna, mRNA sequence.	
DEFINITION	CD437215				
ACCESSION	CD437215.1	GI:31352858			
VERSION	EST.				
KEYWORDS	Zea mays				
SOURCE	Zea mays				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
REFERENCE	1 (bases 1 to 971)				
AUTHORS	Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and Messing,J.				
TITLE	Sequencing of the maize endosperm ESTs				
JOURNAL	Unpublished (2002)				
COMMENT	Contact: Lai, Jinsheng Dr. Joachim Messing's lab				

```

QY 2598 G 2598      773 bp  mRNA  linear  EST 07-NOV-2002
Db 785 G 785

RESULT 3
CA404552
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 773)
Lai, J., Dey, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E. and
Messing, J.
Sequencing of the maize endosperm ESTs
Unpublished (2002)
Contact: Lai, Jinsheng
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq primer: T7.
Location/Qualifiers
1..773
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
/tissue_type="Endosperm of 7-23DAP"
/clone_lib="Endosperm_4"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

FEATURES
source
1..773
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
/tissue_type="Endosperm of 7-23DAP"
/clone_lib="Endosperm_4"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match 28.7%; Score 746.4; DB 14; Length 773;
Best Local Similarity 99.2%; Pred. No. 3.2e-183;
Matches 750; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1646 CGGATATGATATGGCAGGACGATGACCGCGGATTTGGCTTCTTCTGCTGCTCT 1705
Db 18 CGGATATGATATGGCAGGACGATGACCGCGGATTTGGCTTCTTCTGCTGCTCT 77

QY 1706 AGAGTTTCTCTCCAAAGTGGATCTTCCGAAACATATACATGCCATGATGGTCAAG 1765
Db 78 AGAGTTTCTCTCCAAAGTGGATCTTCCGAAACATATACATGCCATGATGGTCAAG 137

QY 1766 TGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1825
Db 138 TGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 197

QY 1826 GGTGATATTCACCATCCCAATCTTGAATTTGGAGCGCATATATGGCAAGCAATGAG 1885
Db 198 GGTGATATTCACCATCCCAATCTTGAATTTGGAGCGCATATATGGCAAGCAATGAG 257

QY 1886 ATATTGTGATAAAGCAACATGCTCTTAATACATATTCAAAGGAAGTGTGAGTCAATGG 1945
Db 258 ATATTGTGATAAAGCAACATGCTCTTAATACATATTCAAAGGAAGTGTGAGTCAATGG 317

QY 1946 TGCCATAGTTCCTCATCTTGGGAATCTATGGCAATCTCAATGAATGATCCGGATAT 2005
Db 318 TGCCATAGTTCCTCATCTTGGGAATCTATGGCAATCTCAATGAATGATCCGGATAT 377

QY 2006 ATGGATCCGTCATGACATCTTATCCCGTCCACATACATCTGTGAGAAATGCTGTTGA 2065

```

Db	66	GTGGTCTCGAATAAAGTGTGGCTGACCTAGTCGAAGGCCTTGTGTCTACTTCCTGG	125
QY	1621	AACCTCAAAATGGAGTGTGGAGTCGGATATGTATATGGCAGGACGATGACCGCCGAT	1680
Db	126	AACCTCAAAATGGAGTGTGGAGTCGGATATGTATATGGCAGGACGATGACCGCCGAT	185
QY	1681	TTGGCTTCTTCTGTGGTCTGTCTGTAGAGTTTCTCTCCAAAGTGGATCTTCTCCGAACA	1740
Db	186	TTGGCTTCTTCTGTGGTCTGTCTGTAGAGTTTCTCTCCAAAGTGGATCTTCTCTTAACA	245
QY	1741	TAATACATTGCCATGATGGTCAAGTGTCTCTGTGGCTACACAAGGAAAACTAG	1800
Db	246	TAATACATTGCCATGATGGTCAAGTGTCTCTGTGGCTACACAAGGAAAACTAG	305
QY	1801	CGAAGCTTAGCTGGCAACGACGGGTGGTATCACCATCCACATCTTGAATTGGAG	1860
Db	306	CGAAGCTTAGCTGGCAAAATGCA CGGGTGGTATTCACCATCCACAATCTTGAATTTGGAG	365
QY	1861	CGCATCATATTGCAAGCAATCAGATATTGTATAAAGCAA CAATGTCTCTTAATACAT	1920
Db	366	CGCATCATATTGCAAAACAAATGAGATATTGTGATAAAGCCACAACATGTCTCTTAATACAT	425
QY	1921	ATTCAAAGGAAGTGTCAAGTTCATGGTGCCCAATGTTCTCTCATTTTGGGAATTTCTATGGCA	1980
Db	426	ATTCAAAGGAAGTGTCAAGTTCATGGTGCCATCGTCTCATCTTGGGAAATTTCTATGGCA	485
QY	1981	TTCTCAATGAATTCATCCGGATATATGGCATCCGTACATATGACAACTTTATCCCGGTCC	2040
Db	486	TTCTCAATGAATTCATCCGGATATATGGCATCCGTACATATGACAACTTTATCCCGGTCC	545
QY	2041	ACTACACTGTGAGAAATGTGGTTCGAAGCCAGAGGGCTGCTAAAGAGGCACTGCAGCAGA	2100
Db	546	ACTACACTGTGAGAAATGTGGTTCGAAGCCAGAGGGCTGCTAAAGAGGCACTGCAGCAGA	605
QY	2101	AGTTTGGGTTACAGCAAAATCGATGTCCCGTCGTAGGAATCGTCACCTGCAGCAGCCC	2160
Db	606	AGTTTGGGTTACAGCAAAATTCATGTCCCGTCGTAGGAATCGTCACCTGCAGCAGCCC	665
QY	2161	AAAAGGGATCCACTCATCAAGCATGCGATTACCGGTACACTCGAAGCGAAACGACAGG	2220
Db	666	AAAAGGGATCCACTCATCAAGCATGCGATTACCGGTACACTCGAAGCGAAACGACAGG	725
QY	2221	TGGTTTTGCTTGGTTCAGCCCGGAC	2246
Db	726	TGGTTTTGCTTGGTTCAGCCCGGAC	751

[illegible]

KEYWORDS	EST.
SOURCE	zea mays
ORGANISM	zea mays
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.

REFERENCE	TITLE
1 (bases 1 to 705) Lai, J., Dey, N., Kim, C.S., Becraft, P., Larkins, E. and Messing, J.	Sequencing of the maize endosperm ESTs

Unpublished (2002)
Contact: Lai, Jinheng
Dr. Joachim Messing's lab
Wakman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@wakman.rutgers.edu
Seg primer: T3.

FEATURES	Location/Qualifiers
source	1..705
	/organism="Zea mays"
	/mol_type="mRNA"
	/cultivar="W22"
	/db_xref="taxon:4577"
	/tissue_type="Endosperm of 7-23DAP"
	/clone_lib="Endosperm_4"
	/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"
ORIGIN	
Query Match	26.3%; Score 683.6; DB 14; Length 705;
Best Local Similarity	98.7%; Pred. No. 7.4e-167;
Matches 689; Conservative	0; Mismatches 9; Indels 0; Gaps 0;
QY	1482 GAGGTATATCTTCCAAAGTACGGTTCGTTGAATCTAAGCAATGTCAAGAATCTACAAATC 154
DB	
QY	8 GGGGTATATCTTCCAAAGTACGGTTCGTTGAATCTAAGCAATGTCAAGAATCTACACATC 67
DB	
QY	1542 CATCAGAGTTTTTCTTGGGGTGGTTCTGAAATAAATGTGTGGGTGGACTAGTCGAGGC 1601
DB	
QY	68 CATCAGAGTTTTTCTTGGGGTGGTTCTGAAATAAAGTGTGGCGTGGACTAGTCGAGGC 127
DB	
QY	1602 CTTTGTGTTTACTTCTGGNACCTCAAAATGGAGTGTTCGGAGTCGGATGTATATATGCG 1661
DB	
QY	128 CTTTGTGTTTACTTCTGGNACCTCAAAATGGAGTGTTCGGAGTCGGATGTATATATGCG 187
DB	
QY	1662 AGGACGATGACCGGATTTGGCTTCTCTGTGCTTCTGCTCTAGAGTTTCTCTCTCCAA 1721
DB	
QY	188 AGGACGATGACCGGATTTGGCTTCTCTGTGCTTCTGCTCTAGAGTTTCTCTCTCCAA 247
DB	
QY	1722 AGTGGATCTTCTCGAACAATAACATGCCATGATTTGGTCAAGTGTCTCTGTGCTGTG 1781
DB	
QY	248 AGTGGATCTTCTCTAACAATAACATGCCATGATTTGGTCAAGTGTCTCTGTGCTGTG 307
DB	
QY	1782 CTACACAGGAAACTACGCGAGTCTAGCTTGGCAACGACGGTGGTATTCCACATC 1841
DB	
QY	308 CTACACAGGAAACTACGCGAAATCTAGCTTGGCAATGCACGGTGGTATTCCACATC 367
DB	
QY	1842 CACATCTTGAATTTGGAGCGCATCATATTGGCAAGCAATGAGATATTGTGATAAGCA 1901
DB	
QY	368 CACATCTTGAATTTGGAGCGCATCATATTGGCAAGCAATGAGATATTGTGATAAGGC 427
DB	
QY	1902 ACACTGTCTCTAATACATATTCAAGGAAGTGTCAAGTCAAGTGGCATAGTTCCTCAT 1961
DB	
QY	428 ACACTGTCTCTAATACATATTCAAGGAAGTGTCAAGTCAAGTGGCATAGTTCCTCAT 487
DB	
QY	1962 CTTGGGAATCTATGGCAATCTCAATGGAAATTCATCCGGATATATCGGATCCGTACAAT 2021
DB	
QY	488 CTTGGGAATCTATGGCAATCTCAATGGAAATTCATCCGGATATATGGGAATCCGTACAAT 547
DB	
QY	2022 GNCACATTTATCCCGTCCACTACACTGTGCAGAAATGTGGTGTGAAGCAAGAGGGCTGCT 2081
DB	
QY	548 GACAACTTTATCCCGTCCACTACACTGTGCAGAAATGTGGTGTGAAGCAAGAGGGCTGCT 607
DB	
QY	2082 AAGAGGGCACTGCAGCAGAAGTTTGGGTTCACAGAAATCGAATGCCCGTCTGTAGGAATC 2141
DB	
QY	608 AAGAGGGCACTGCAGCAGAAGTTTGGGTTCACAGAAATTCATGTATGTCCCCGTCTGTAGGAATC 667
DB	
QY	2142 GTCACTGCGCTGACAGGCCAAAGGGATCCACCTGAT 2179
DB	
QY	668 GTCACTGCGCTGACAGGCCAAAGGGATCCACCTGAT 705
DB	

RESULT 6	CD434207	CD434207	652 bp	mRNA	linear	EST 03-JUN-2003
LOCUS	CD434207	EL01N0320B09.b	Endosperm_3	Zea mays	cdna, mRNA	sequence.
DEFINITION	CD434207	CD434207.1	GI:31349850	EST.	KEYWORDS	
ACCESSION	CD434207	CD434207.1	GI:31349850	EST.	KEYWORDS	
VERSION	CD434207.1	CD434207.1	GI:31349850	EST.	KEYWORDS	
SOURCE	CD434207	CD434207.1	GI:31349850	EST.	KEYWORDS	

ORGANISM	Zea mays		QY	605 ATTTGATTATACATAAACTCAAGACCTCTAGTTCCAGTACTGAGATATGATGATCATGG 564		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.			601 ATTTGATTATACATAAACTCAAGACCTCTAGTTCCAGTACTGAGATATGATGATCATGG 660		
AUTHORS	Lai, J., Dey, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E. and Messing, J.			QY	665 TGGCTATACAAATGGATTGATGGACTCTCTT 696	
TITLE	Sequencing of the maize endosperm ESTs				661 TGGCTATACAAATGGATTGATGGACTCTCTT 692	
JOURNAL	Unpublished (2002)			Db		
COMMENT	Contact: Lai, Jinsheng Dr. Joachim Messing's lab Waksman Institute, Rutgers University 190 Frelinghuysen Rd., Piscataway, NJ 08854, USA Tel: 732-445-3801 Fax: 732-445-5735 Email: jlai@waksman.rutgers.edu Seq primer: T3.					
FEATURES	Location/Qualifiers			RESULT 7	CA195121	
source	1..692				CA195121	
	/organism="Zea mays"			LOCUS	SCAGSB1089G09.g SB1 Saccharum officinarum cDNA clone SCAGSB1089G09	
	/mol_type="mRNA"				5' mRNA sequence.	
	/cultivar="W22"			ACCESSION	CA195121	
	/db_xref="taxon:4577"				CA195121.1 GI:35223049	
	/tissue type="Endosperm of 7-23DAP"			VERSION	EST.	
	/clone_lib="Endosperm 3"				Saccharum officinarum	
	/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"			KEYWORDS	Saccharum officinarum	
					Saccharum officinarum	
ORIGIN	Query Match			ORGANISM	Saccharum officinarum	
	Best Local Similarity 98.7%; Pred. No. 2.7e-165;				Saccharum officinarum	
	Matches 693; Conservative 0; Mismatches 9; Indels 0; Gaps 0;			Saccharum officinarum		
QY	5 TCGTGAATAAATATTCGCTGGAAACAGTGTGTTTACTATCCAGATGATTGAAAGC 64			REFERENCE	1 (bases 1 to 579)	
Db	1 TCGTGAATAAATATTCGCTGGAAACAGTGTGTTTACTATCCAGATGATTGAAAGC 60				Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.	
QY	65 TGATTCACAAATGATCTCTATTTCATCTGATCTATCAGCTGTGCCAATGAGCTGA 124			AUTHORS	The libraries that made SUCSEST	
Db	61 TGATTCACAAATGATCTCTATTTCATCTGATCTATCAGCTGTGCCAATGAGCTGA 120				Genet. Mol. Biol. 24 (1-4), 1-7 (2001)	
QY	125 TGTACTTATCAAGGAGCATTCATAGGGTGGAGTGGAGATTTTCTCACTGAAAATGCA 184			JOURNAL	Contact: Arruda P	
Db	121 TGTACTTATCAAGGAGCATTCATAGGGTGGAGTGGAGATTTTCTCACTGAAAATGCA 180				Centro de Biologia Molecular e Engenharia Genetica	
QY	185 CAAGAGCGAGCTGCAGGGGACTCGTGTCTGCAAACTATACATTCCTAAGCAGGCATA 244			COMMENT	Universidade Estadual de Campinas	
Db	181 CAAGAGCGAGCTGCAGGGGACTCGTGTCTGCAAACTATACATTCCTAAGCAGGCATA 240				Caixa Postal 6010, 13083-970, Campinas SP, Brazil	
QY	245 CAGATGACCTTGTGTTTTTAAACGACACACACGGTATATGAAATATATCAATATGA 304			FEATURES	Tel: 55 19 3788 1137	
Db	241 CAGATGACCTTGTGTTTTTAACTTTTACGGTATATGAAATATATCAATATGA 300				Fax: 55 19 3788 1089	
QY	305 TTTCGTGATACAAATAGAAAACCACTGGATGAAAATTTATTTGAGGATTTCTTGGCTGA 364			source	Email: parruda@unicamp.br	
Db	301 TTTCGTGATACAAATAGAAAACCACTGGATGAAAATTTATTTGAGGATTTCTTGGCTGA 360				Clone distribution: clone distribution information can be found	
QY	365 AGAAAAGCAACGAGACTTGAGAACTTGCAAACTGAGGAAGCTGAAAGGAGGAGCAAAAC 424			LOCATION/Qualifiers	through the Brazilian Clone Collection Center (BCCC) at	
Db	361 AGAAAAGCAACGAGAACTTGAGAACTTGCAAACTGAGGAAGCTGAAAGGAGGAGCAAAAC 420				http://www.bcccenter.fcav.unesp.br	
QY	425 TGATGAGCAGCGCGAATGGAGAAAGAAAGGCGCGAGATAAAGCTGACAGGGTACAAGC 484			Seq primer: T7 Promoter Primer.	plate: 089 row: G column: 09	
Db	421 TGATGAGCAGCGCGAATGGAGAAAGAAAGGCGCGAGATAAAGCTGACAGGGTACAAGC 480				Seq primer: T7 Promoter Primer.	
QY	485 CAAAGTTGAGGTAGAGACGAAAGAAATTAATTTGCAATGATGTTTGGGTTTAGCCAGAGC 544			Location/Qualifiers	1..579	
Db	481 CAAAGTTGAGGTAGAGACGAAAGAAATTAATTTGCAATGATGTTTGGGTTTAGCCAGAGC 540				/organism="Saccharum officinarum"	
QY	545 TCCTGTTGATTAATTTATGTAATTCAGCCCATCAGGACTGGACAGAGGCTTACTGTCTCAG 604			/mol_type="mRNA"	/db_xref="taxon:4547"	
Db	541 TCCTGTTGATTAATTTATGTAATTCAGCCCATCAGGACTGGACAGAGGCTTACTGTCTCAG 600				/clone="SCAGSB1089G09"	
				/lab_host="DH10B"	/clone_lib="SBI"	
					/note="Organ: Stalk Bark from adult plants; Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [Stalk Bark from adult plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CI-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucsest.lad.ic.unicamp.br/public"	
				Query Match	20.2%; Score 523.8; DB 14; Length 579;	
					Best Local Similarity 95.2%; Pred. No. 3.3e-125;	
				Matches 551; Conservative 0; Mismatches 27; Indels 1; Gaps 1;		
QY	833 CAATGGAGGACATGATTTTCATGCTACCCCTCCAAATAACATGACTGAGAGAGTATTG 892				Db	1 CAATGGAGGACATGATTTTCATGCTACCCCTCCAAATAACATGACTGAGAGAGTATTG 60
Db	893 GATGGAAGAAAGCAAAAGGATCTATACAGGCTTCAACAGAGAGGAGGAAAGGGAGGA 952			QY		61 GATGGAAGAAAGCAAAAGGATCTATACAGGCTTCAACAGAGAGGAGGAAAGGGAGGA 120
QY	953 GCCTATTAAAGAGGAGCTGAGAGAAATGCAAAATGAAAAGCTGAGATGAAGAAAGAC 1012				Db	953 GCCTATTAAAGAGGAGCTGAGAGAAATGCAAAATGAAAAGCTGAGATGAAGAAAGAC 180
Db	121 GCCTATTAAAGAGGAGCTGAGAGAAATGCAAAATGAAAAGCTGAGATGAAGAAAGAC 180					

QY	1013	TATGAGATGTTCTCGGTTTCTCAGAAACACATGTTTACACCGAACCACTTGAATACA	1072
Db	181	TATGAGATGTTCTCGGTTTCTCAGAAACACATGTTTACACTGAACCACTTGAATACA	240
QY	1073	TGCTGGAACTAC-TATTGATGTGCTTTATTAATCTCTTAATACAGTTCTTAATCGAAGC	1131
Db	241	TGCTGMAACTACGTGGAGGTGGCTTTATAATCTCTTAATACACAGTGTAACTGGAAGC	300
QY	1132	CAGAGTTTGGTTTCGATGTTCTTAAATCGTTGATGTATCCAGGTGGGTGTTGCCAC	1191
Db	301	CAGAGTTTGGTTTCGATGTTCTTAAATCGTTGATGTATCCAGGTGGGTGTTGCCAC	360
QY	1192	CTCAGAAGATGGTCAACAGCAGAAATGGTTTACACCTAAAGCAACAGTTTACGTTCCAC	1251
Db	361	CTCAGAAGATGGTCAACAGCAGAAATGGTTTACACCTAAAGCAACAGTTTACGTTCCGC	420
QY	1252	GAGATGCTTATGATGACATTCGTTTCTCGAGTTCAGAGAGGTGGAATTTATGATA	1311
Db	421	AAAGTGCCTATATGATGACATTCGTTTCTCGAGTTCAGAGAGGTGGAATTTATGATA	480
QY	1312	ACAGAAATGGTTAGACTATCATATTCCTGTTTCTCGAGTTCAGAGAGGTGGAATTTATGATA	1371
Db	481	ACAGAAATGGTTAGACTATCATATTCCTGTTTCTCGAGTTCAGAGAGGTGGAATTTATGATA	540
QY	1372	TGCACATTTGCCATATGCTGTTTGAGATGGCACCAATCG	1410
Db	541	TGCACATTTGCCATATGCTGTTTGAGATGGCACCAATCG	579
RESULT 8			
CF051954/c			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
Genoplante, a major partnership french program in plant genomics Unpublished (2003)			
Contact: Genoplante			
Genoplante			
93, rue Henri Rochefort 91025 EVRY CEDEX France			
Tel: 33 1 69 47 54 00			
Fax: 33 1 69 47 54 10			
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com) and http://genoplante-info.infobiogen.fr .			
FEATURES			
Location/Qualifiers			
1..535			
/organism="Zea mays"			
/mol_type="mRNA"			
/cultivar="F2"			
/db_xref="taxon:4577"			
/clone="QCM33a07"			
/tissue_type="apex"			
/clone_lib="QCM"			
ORIGIN			
Query Match 20.0%; Score 519.8; DB 14; Length 535;			
Best Local Similarity 99.6%; Pred. No. 3.6e-124;			
Matches 521; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	1494	CCAAAGTACGGTTGCTGAATCTAAGCAATGTCAAGATCTCAAAATCCATCAGATTTT	1553
Db	523	CCGAGTACGGTTGCTGAATCTAAGCAATGTCAAGATCTCAAAATCCATCAGATTTT	464

QY	1554	TCCTGGGTGGTTCTGAATAAATGTTGCGCTGGACTAGTCGAAGGCCCTTTGTTTAC	1613
Db	463	TCCTGGGTGGTTCTGAATAAATGTTGCGCTGGACTAGTCGAAGGCCCTTTGTTTAC	404
QY	1614	TTCTGGAACTCAAAATGGGATGTTTGGAGTCGGATATGATATGCGGAGCATGAC	1673
Db	403	TTCTGGAACTCAAAATGGGATGTTTGGAGTCGGATATGATATGCGGAGCATGAC	344
QY	1674	CGCCGATTGGCTTCTCTGCTGCTCTAGAGTTTCCTCCCAAAGTGGATCTTCT	1733
Db	343	CGCCGATTGGCTTCTCTGCTGCTCTAGAGTTTCCTCCCAAAGTGGATCTTCT	284
QY	1734	CCGAACATAATACATGTCATGATTGGTCAAGTCTCTCTGCTGCTGCTACACAAGAA	1793
Db	283	CCGAACATAATACATGTCATGATTGGTCAAGTCTCTCTGCTGCTGCTACACAAGAA	224
QY	1794	AACTACGGGAAGTCTAGCTTGGCAAAACGACGGGTGGTATTCACCATCCAAATCTTCAA	1853
Db	223	AACTACGGGAAGTCTAGCTTGGCAAAACGACGGGTGGTATTCACCATCCAAATCTTCAA	164
QY	1854	TTTGGAGCGCATCATATTGGCAAAACGACGGGTGGTATTCACCATCCAAATCTTCAA	1913
Db	163	TTTGGAGCGCATCATATTGGCAAAACGACGGGTGGTATTCACCATCCAAATCTTCAA	104
QY	1914	AATACATATTCAAAGGAAGTGTCAAGTCAATGTCATGTCGATGTCCTCTCTCTCTCT	1973
Db	103	AATACATATTCAAAGGAAGTGTCAAGTCAATGTCATGTCGATGTCCTCTCTCTCTCT	44
QY	1974	TATGGCATCTCAATGGGAATGATCGGATATATGGGATCCGT	2016
Db	43	TATGGCATCTCAATGGGAATGATCGGATATATGGGATCCGT	1

RESULT 9			
CD433067			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
Sequencing of the maize endosperm ESTs Unpublished (2002)			
Contact: Lai, Jinsheng			
Dr. Joachim Messing's lab			
Waksman Institute, Rutgers University			
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA			
Tel: 732-445-3801			
Fax: 732-445-5735			
Email: jlai@waksman.rutgers.edu			
Seq primer: T3.			
FEATURES			
Location/Qualifiers			
1..571			
/organism="Zea mays"			
/mol_type="mRNA"			
/cultivar="W22"			
/db_xref="taxon:4577"			
/tissue_type="Endosperm_3"			
/clone_lib="Endosperm_3"			
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"			
ORIGIN			
Query Match 19.8%; Score 517.4; DB 14; Length 571;			
Best Local Similarity 95.3%; Pred. No. 1.6e-123;			
Matches 544; Conservative 0; Mismatches 26; Indels 1; Gaps 1;			

```

/mol_type="mRNA"
/cultivar="CO328"
/db_xref="taxon:4577"
/clone="Zm03_06d02"
/tissue_type="leaf, crown"
/def_stage="4-leaf"
/clone_lib="Zm03_AAFV_ECORC_cold_stressed_maize_seedlings"
/clone="Zm03_AAFV_ECORC_cold_stressed_maize_seedlings"
/site="Eco RI"
/notes="Bluescript SK+/XhoI-EcoRI; Site 1: Eco RI;
Site 2: Xho I; Corn seedlings at 4-leaf stage were exposed
to low temperature/high light (100C/700-800uE/m2/s) for 4
days. Plants were grown/treated by J. Simmonds/L. Cass.
Library prepared by C. Piche using Stratagene kit."

```

ORIGIN

```

Query Match      19.9%; Score 517.4; DB 12; Length 831;
Best Local Similarity 98.5%; Pred. No. 1.8e-123;
Matches 543; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

QY 2048 TTGTGAGATGTGTGTAAGGCAAGAGGGCTGCTAAGAGGGGCTGACGACGAGCTTTGG 2107
DB 831 TTGTGAGATGTGTGTAAGGCAAGAGGGCTGCTAAGAGGGGCTGACGACGAGCTTTGG 773
QY 2108 GTTACAGCAATCGATGTCCTCGTCTAGGATCGTCACTCGCTCGACGACGAGCTTTGG 2167
DB 772 GTTACAGCAATCGATGTCCTCGTCTAGGATCGTCACTCGCTCGACGACGAGCTTTGG 713
QY 2168 GATCCACCTGATCAAGCATGCGATTCACCGTACCTCGAAGCGGACGAGCTTTGG 2227
DB 712 GATCCACCTGATCAAGCATGCGATTCACCGTACCTCGAAGCGGACGAGCTTTGG 653
QY 2228 GTTGTGTTGAGCGCGGCTGCTGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 2287
DB 552 GTTGTGTTGAGCGCGGCTGCTGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 593
QY 2288 CACGCGGTAAACCATGGGCAAGTGGGCTTCTGATTCGATTCGATTCGATTCGATTCG 2347
DB 592 CACGCGGTAAACCATGGGCAAGTGGGCTTCTGATTCGATTCGATTCGATTCGATTCG 533
QY 2348 TCTGATATACGCTGGCTGCTGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 2407
DB 532 TCTGATATACGCTGGCTGCTGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 474
QY 2408 AACTCAGCTCGTCCGATGGGCTGATGGAACCATTCGATTCGATTCGATTCGATTCG 2467
DB 473 AACTCAGCTCGTCCGATGGGCTGATGGAACCATTCGATTCGATTCGATTCGATTCG 414
QY 2468 CTTTCGACATGCTCTTCGATGTCGATTCGATTCGATTCGATTCGATTCGATTCG 2527
DB 413 CTTTCGACATGCTCTTCGATGTCGATTCGATTCGATTCGATTCGATTCGATTCG 354
QY 2528 GCCCAACGGGTTTACGCTTTCGAGGAGCTGATGCAACGGGTTTACGCTTTCGAGG 2587
DB 353 GCCCAACGGGTTTACGCTTTCGAGGAGCTGATGCAACGGGTTTACGCTTTCGAGG 294
QY 2588 GCGGATCTCAG 2598
DB 293 GCGGATCTCAG 283

```

RESULT 11

```

LOCUS CK247929
DEFINITION Solanum tuberosum callus cDNA library, normalized and full-length
ACCESSION CK247929
VERSION CK247929.1
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 1014)

```

```

1302 ATTATGATATACAGAAATGGGTAGACTATCATATCTCTGTTTGGTCAATTCGAAAG 1361
DB 1 ATTATGATATACAGAAATGGGTAGACTATCATATCTCTGTTTGGTCAATTCGAAAG 60
1362 GAACACCTATGTCACATTCGTCACATTCG-TCTGTGAGATGTCACCAATTCGCAAGTTGG 1420
DB 61 GAACACCTATGTCACATTCGTCACATTCG-TCTGTGAGATGTCACCAATTCGCAAGTTGG 120
QY 1421 AGGCTCTGTGATGTGTCATAGTCTTTACGCTGCTGCAAGATTTAGGACACAAATGT 1480
DB 121 AGGCTCTGTGATGTGTCATAGTCTTTACGCTGCTGCAAGATTTAGGACACAAATGT 180
QY 1481 GGAGGTATCTTCCAAAGTGGTGTGATCTAAGCAATGTCAAGAAATCTCAAAAT 1540
DB 181 GGAGGTATCTTCCAAAGTGGTGTGATCTAAGCAATGTCAAGAAATCTCAAAAT 240
QY 1541 CCATCAGAGTCTTTCTGCGGTTGTTCTGAAATAAATGTTGGCGTGGACTAGTCGAAG 1600
DB 241 CCATCAGAGTCTTTCTGCGGTTGTTCTGAAATAAATGTTGGCGTGGACTAGTCGAAG 300
QY 1601 CTTTGTGTTTACTTCTCGAAGCTCAAAATGGGATGTTGGAGTCGATATGTAATCG 1660
DB 301 CTTTGTGTTTACTTCTCGAAGCTCAAAATGGGATGTTGGAGTCGATATGTAATCG 360
QY 1661 CAGGAGGATGACCGGATTTGGCTTCTCTGCTGTTCTGCTCTAGAGTTCTCTCCA 1720
DB 361 CAGGAGGATGACCGGATTTGGCTTCTCTGCTGTTCTGCTCTAGAGTTCTCTCCA 420
QY 1721 AAGTGGATCTTCTCGAACAATAATGATGCGATGTTGTCAGTCTGCTCTGCTGCTG 1780
DB 421 AAGCGGATCTTCTCGAACAATAATGATGCGATGTTGTCAGTCTGCTCTGCTGCTG 480
QY 1781 GTTACACAGAAACTACCGAGTCTAGCTGGCAAGCGCGGTGCTGATTCACCAT 1840
DB 481 GTTACACAGAAACTACCGAGTCTAGCTGGCAAGCGCGGTGCTGATTCACCAT 540
QY 1841 CCACAACTTGAATTTGGAGCGCATCATATT 1871
DB 541 CCACAACTTGAATTTGGAGCGCATCATATT 571

```

```

RESULT 10
LOCUS BG319783
DEFINITION BG319783 831 bp mRNA linear EST 27-FEB-2001
ACCESSION BG319783
VERSION BG319783.1
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 831)
Simmonds, J.A., Singh, J.A., Piche, C., Cass, L., Couroux, P., De
Moors, A., Harris, L.J., Hattori, J.I., Quillet, T., Robert, L.S.,
Spott, D., and Tinker, N.A.
Expressed Sequence Tags from Cold-Stressed Maize Seedlings Grown
Under High Light Intensity
Unpublished (2001)
Contact: Singh, J.A.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
0C6, Canada
Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@agr.ca.
Location/Qualifiers
1. 831
/organism="Zea mays"

```

FEATURES

source

Mon Jun 21 12:19:28 2004

AUTHORS
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
TITLE
Generation of ESTs from potato callus tissue
JOURNAL
Unpublished (2003)
COMMENT
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: Art TAG GTC ACA CTA TAG.

FEATURES
source
1. .1014
Location/Qualifiers
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="kennebec"
/db_xref="taxon:4113"
/clone="POCAX21"
/tissue_type="callus"
/lab_host="DH108-Tona"
/clone_lib="potato callus cDNA library, normalized and full-length"
/notes="vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Solanum tuberosum var. kennebec callus tissue grown on solid media."

ORIGIN
Query Match 18.8%; Score 488.4; DB 14; Length 1014;
Best Local Similarity 68.9%; Pred. No. 7.1e-116;
Matches 699; Conservative 0; Mismatches 311; Indels 4; Gaps 2;
QY 1328 CTATCATATTCCTGTTTGGTCAATTCGAAAGAACCACTATGACATGTCACAT 1387
DB 1 CTATCATATTCCTGTTTGGTCAATTCGAAAGAACCTCAATGCAATATGTCATAT 60
QY 1388 TGCTGTTGAGATGGCCAAATCGAAAGTTGGAGCTCTTGGTGTATGTCACATGCT 1447
DB 61 TGCTGCGAAATGGCCAAATTCGAAAGTTGGAGGCTCTTGGTGTATGTCACATGCT 120
QY 1448 TTCAGCTGTTGCAAGATTAGGACACATGTCGAGGTTATCTTCCAAAGTACGGTTG 1507
DB 121 TTCCTGCTGCTGTTCAAGATTAAACCATTAATGTCATATTAATCTTACCTAAGTATGCTG 180
QY 1508 CTTGAATTAAGCAATGTCAGAAATCTCAATATCAATATCAATATCAATATCAATATCA 1567
DB 181 TTGAGATGATTAATGTCAGAAATCTCGGTTTCAAAAGTACTTTTGGGTTGGGAC 240
QY 1568 TGAATTAATGTCGCTGGTGGTACTGTCGAGGCTTTGGTGTATGTCACATGCTCA 1627
DB 241 TGAATTAAGTATGTTTGGAAAGTGGAGGTCCTCTCGGTTCTATTTTGGAGCTCA 300
QY 1628 AATGGATGTTGGAGTGGATGATATGATGGCAGGAGATGACCGC---CGATTGG 1684
DB 301 AATGGGTTATTTTCGAAAGGTCGATATGTTGTCAGCAATGATGTCGAAAGTTGG 360
QY 1685 CTTCTCTGCTGCTCTGCTCTAGATTTCTCTCCAAAGTGGATCTTCTCGGACATAT 1744
DB 361 TTTCTCTGTCACGCGCTTTGGAGTTCTCTCTGCAAGTGGATTTAGTCGGGATATCAT 420
QY 1745 ACATGTCATGTTGTCAGTCTGCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCT 1804
DB 421 TCATGTCATGTTGTCAGTCTGCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCT 480
QY 1805 GTCTAGCTTGGCAACGACCGGGTGTATTCACCATCCACATCTGTAATTTGAGGCGCA 1864
DB 481 CTATGTCATGTCAGCAATCTGTCATGTCCTTACGATACATATCTTGAATTTGGGCGCA 540
QY 1865 TCATATTCGCAAGCAATGAGATATTTGTAATAAGCAACATGTCCTATACATATTC 1924
DB 541 TCTCATTTGGAGAGCAATGACCTAACCGCAGACAAAGCTACACAGTTTCACCACTATCTC 600
QY 1925 AAGGAAGTGTGAGTGTGTCAGTGTGTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1984
DB 601 ACAGGAGGTGTCTGGAACCCCTGTAATTCGCTCTCACCTTTCACAGTTCCATGTTAGT 660

QY 1985 CAATGGAATTCATCCGGATATATGGATCCGTAATGACAACTTTATCCCGTCCACTA 2044
DB 661 GAATGGGATTCACCCAGATATTTGGGATCCCTTTAAACGATAAGTTTCATTCGATCCATA 720
QY 2045 CACTTGTGAGATGTTGTTGAGGCGGCTGCTTAAGAGGCGACATGTCAGCAGAAGTT 2104
DB 721 CACTTCAGAAACGTTGTTGAGGCGGCTGCTTAAGAGGCGACATGTCAGCAGAAGTT 780
QY 2105 TGGGTTACAGCAATTCGATGTCCTGCTGCTAGGAATGCTGCTGCTGCTGCTGCTGCTGCT 2164
DB 781 TGGACTGAAACAGGCTGACCTTCTTGTGTAAGTAATTAACCTGCTGCTGCTGCTGCTGCT 840
QY 2165 GGGGATCCACCTGATCAAGATGCGATTCACCTGACCTGACCTGACCTGACCTGACCTGACCT 2224
DB 841 AGAATCCACCTCATTAACATGCTATTTGGGCGACCTTTGGAACGGAACGACGATGT 900
QY 2225 TTTGCTGTTGTCAGCGCGGACTCTGATCAAGCTGA-TTTTGTCAACCTTGGCGAATA 2283
DB 901 CTTGCTTGGTCTGCTCTGCTGATCTTGGGCGACCTTTGGAACGGAACGACGATGT 960
QY 2284 CGCTCCAGCGGTAAACCATGGCAAGTGGAGGCTTTCTTGGACCTGACGAGAC 2337
DB 961 AATGTCATCCCAATATATATGACCGCGCAGGACTCTGCTTAACATATGACGAGC 1014

RESULT 12
BZ970127/c 638 bp DNA linear GSS 25-MAR-2003
LOCUS BZ970127 ZM 0.6_1.0_KB Zea mays genomic clone ZMBTa379013,
DEFINITION genomic survey sequence.
ACCESSION BZ970127
VERSION BZ970127.1 GI:29190595
KEYWORDS GSS, Zea mays
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 638)
AUTHORS Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
TITLE Maize Genomics Consortium
JOURNAL Unpublished (2003)
COMMENT Other GSSs: PUGM91TB
Contact: Cathy Whitelaw
TIGR Medical Center Drive, Rockville, MD 20850, USA
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.

FEATURES
source
1. .638
Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMBTa379013"
/clone_lib="ZM 0.6_1.0_KB"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high Cot selected genomic DNA library"

ORIGIN
Query Match 18.1%; Score 470.6; DB 28; Length 638;
Best Local Similarity 97.2%; Pred. No. 2.6e-111;
Matches 479; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 265 TTAACGACACACCGGTATATGAAAATAATACAAATAATGATTTCTGTATACAAATAGAA 324
DB 638 TTAACGACACACCGGTATATGAAAATAATACAAATAATGATTTCTGTATACAAATAGAGC 579

/note="Vector: pCMV.SPORT6; Crown and developmental stages of spike formation in wheat cultivar Norstar. 4 mRNA populations were combined before constructing the library. The first mRNA population is from 1cm crown sections after 30 days of cold acclimation. The second is from 1cm crown sections after 11 days of deacclimation (before deacclimation plants were fully vernalized for 49 days). The third is from different developmental stages of spike formation (5 to 50mm) that still have not emerged from the leaf (dissection required). The last is from different developmental stages of spike and seed formation after having emerged from the leaf (visible). First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI."

ORIGIN

Query Match	17.8%;	Score	463.6;	DB	14;	Length	1042;
Best Local Similarity	70.5%;	Pred. No.	2.1e-109;				
Mismatches	633;	Conservative	0;	Mismatches	264;	Indels	1;
Gaps	1;						
QY	56	ATTGAAGCTGATTCACAAATTCATCTCTATTTCAATCGTGATCTATCAAGTGTGGCAA	115				
DB	8	AATGGTTGGAGATGGAAACCAATTAATGCCCTTTGATACGGATATCAATGTTGCTTGTCT	67				
QY	116	TGAGCTGTATGTTATCAAAAGGAGCATTCATGGGTGGAAGTGGAGATTTTCACTGA	175				
DB	68	AAGGGGAGGATGCTTATCAAAAGGGCATTCATGGTTGGAGATGGAACCATTTCACTGA	127				
QY	176	AAAAATTCACAAAGCGAGCTGGCGAGGGAGCTGGTGTCTGCAAACTATACATTTCTTAA	235				
DB	128	AAAAATTCATAGAAAGTGAATTAACAGGGGATTTGGTGTGTTTAAAGCTCTACCTACCCA	187				
QY	236	GCAGCATACAGATGGACTTTGTGTTTAAACGGACACACGGGTATATGAAATAATAA	295				
DB	188	GCAGCATACAGATGGACTTTGTGTTTAAACGGACACACGGGTATATGAAATAATAA	247				
QY	296	CAATAATGATTCGTGTATACAAATAGAAAGCACCATGATGAAATTTATTGGAGATT	355				
DB	248	TTATATGATTTGCTCTGTCATATAGAAAGTGAAGGGGATGAACACTCATTTGGAGCT	307				
QY	356	CTTGCTGAAAGAAAGCAACGAGACTTGAACCTTCMAATAGGAGCTGAAAGAG	415				
DB	308	CTTGCTGAAAGAAAGCAACGAGACTTGAACCTTCMAATAGGAGCTGAAAGAG	367				
QY	416	GAGCAAACTGATGACGAGCGGCAATGGAGGAAGAAAGGGCCGAGATAAGCTGACAG	475				
DB	368	AAGCAAGCCGAGGAGGAGCGCGGAGGAGAAAGGGCCGCAATGGAGGCTGACAG	427				
QY	476	GGTACAAAGCAAGGTTGAGGTAGACGAGAGAAATTAATTTGCAATGTTTGGTTT	535				
DB	428	GGCAGAGGCAAAAGCTGAGGTTGAGACGAGGAGGAAATTAATTTGCAATGTTTGGTTT	487				
QY	536	AGCCAGAGCTCTGTTGATAATTTATGTTGATGAGCTCTCTTTGCTGAAAGGCTTCTCA	595				
DB	488	AGCCAGAGCTCTGTTGATAATTTATGTTGATGAGCTCTCTTTGCTGAAAGGCTTCTCA	547				
QY	596	TACTGTGAGATTTGATTAATAACATTAATCAAGACCTCTAGTTCAAGTCTGAGTATG	655				
DB	548	TAGGTCAGATTTGATTAATAACATTAATCAAGACCTCTAGTTCAAGTCTGAGTATG	607				
QY	656	GATGTCAGTGGTGTATTAACAAATTTGATGAGCTCTCTTTGCTGAAAGGCTTCTCA	715				
DB	608	GTTCATGAGGTTTACAAATCACTGAGTCTGATGGGCTCTTATTTGAGAGACTAGTCAA	667				
QY	716	TCATCATGACAAAGATTTGATTTGGTGTGAGATTTGTCAGATTTGTCCTGCAAAACATA	775				
DB	668	ATCTGAAGAACAGATGGTGTGATTTGGTGTATGAAATTTTACTCTACCTGAAGGCAATT	727				
QY	776	TGTTATGAGCTGGGTTTCTCTGACGGCCCAACAGGAGTGCAGGAAATTTATGACACAA	835				
DB	728	GGTGTAGGACTGCGTATTAGTCTGATGATCCCTGGGAGCGCAAGTATGATATAACA	787				

QY	325	GCACCATGATGAAAAATTTATTTAGGATTTCTTGCTGAAGAAAGCAACGAGAACTTG	384				
DB	578	ACCCATGATGAAATTTATTTAGGATTTCTTGCTGAAGAAAGCAACGAGAACTTG	519				
QY	385	AGAACCTTGAATGAGGAAAGCTGAAAGGAGGACAAACTGATGAGCGCGGAATGG	444				
DB	518	AGAACCTTGAATGAGGAAAGCTGAAAGGAGGAGACAAACTGATGAGCGCGGAATGG	459				
QY	445	AGAGAAAGGGCGGAGATAAAGCTCACAGGGTACAAAGCCAAAGGTTGAGGTAGACGA	504				
DB	458	AGAGAAAGGGCGGAGATAAAGCTCACAGGGTACAAAGCCAAAGGTTGAGGTAGACGA	399				
QY	505	AGAAGATAAATTTGTCATTTGTTGGTTAGCCAGAGCTCTCTGTTGATAATTTATGGT	564				
DB	398	AGAAGATAAATTTGTCATTTGTTGGTTAGCCAGAGCTCTCTGTTGATAATTTATGGT	339				
QY	565	ACATTGAGCCCATCAGACTGGACAGAGCTACTGTCAGATTTCTATTATAACATAAACT	624				
DB	338	ACATTGAGCCCATCAGACTGGACAGAGCTACTGTCAGATTTCTATTATAACATAAACT	279				
QY	625	CAAGACCTCTAGTTTACAGTACTGAGATATGATGATGATGATGATGATGATGATGATG	684				
DB	278	CAAGACCTCTAGTTTACAGTACTGAGATATGATGATGATGATGATGATGATGATGATG	219				
QY	685	ATGAGCTCTCTTTGCTGAAAGGCTTGTTCATCATCATGACAAAGATTTGATTTGGT	744				
DB	218	ATGAGCTCTCTTTGCTGAAAGGCTTGTTCATCATCATGACAAAGATTTGATTTGGT	159				
QY	745	TTGAGATGTTGT 757					
DB	158	TTGTAGATGGTAT 146					
RESULT 13							
LOCUS	CK207070	1042 bp	mRNA	linear	EST 08-DEC-2003		
DEFINITION	FGAS018685 Triticum aestivum FGAS: Library 5 GATE 7 Triticum						
ACCESSION	aestivum cDNA, mRNA sequence.						
VERSION	CK207070						
KEYWORDS	EST.						
SOURCE	Triticum aestivum (bread wheat)						
ORGANISM	Triticum aestivum						
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;						
AUTHORS	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;						
	Poideae; Triticeae; Triticum.						
	1 (bases 1 to 1042)						
	Allard, F., Crosby, M.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,						
	Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,						
	Links, M.G., McCarthy, B.L., Monroy, A., Muzak, I., Nilson, D.,						
	Penniket, C., Roach, J.L. and Sarhan, F.						
	Functional Genomics of Abiotic Stress In Wheat and Canola Crops						
	Unpublished (2003)						
TITLE	Contact: Wm. L. Crosby						
JOURNAL	Bioinformatics						
COMMENT	University of Saskatchewan, Department of Computer Science						
	1C101 Engineering Building, 57 Campus Drive, Saskatoon,						
	Saskatchewan, S7N 5A9, Canada						
	Tel: 306 966 1769						
	Fax: 306 966 2033						
	Email: fgas_est@cs.usask.ca						
	This sequence is the direct result of the Base calling software						
	Phred (default parameters). It is the raw base calls. To aid in the						
	identification of the high quality insert the software Lucy						
	(default parameters) has been run on this sequence. Lucy identified						
	the region [16,824].						
FEATURES	Plate: LSB009 row: I column: 20.						
source	Location/Qualifiers						
	1..1042						
	/organism="Triticum aestivum"						
	/mol_type="mRNA"						
	/db_xref="taxon:4565"						
	/clone_lib="Triticum aestivum FGAS: Library 5 GATE 7"						

836 TGGAGGACATGATTTCATCTACCTCCAAATAAATGATCTGAGGAAGATTTGGAT 895
 788 TGGGAGCAAGATTTCATCTGCGCGTTCAAGAGCATATCCGATGCTTGTCTGGGT 847
 896 GGAAGAGAAACAAGGATCTATACAGGCTTCAACAGAGAGGAGGAAAGGAGGAG 953
 848 GAAAGAGAGAGTAGGATAT-TTGAAGGCTTCAACGAAAAAATAAAGGCGCG 904

RESULT 14
 CD436069/c
 LOCUS EL01N0370A09.b Endospem_3 Zea mays cDNA, mRNA sequence. EST 03-JUN-2003
 DEFINITION CD436069
 ACCESSION CD436069.1 GI:31351712
 VERSION CD436069.1
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 791)
 Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and Messing,J.
 Sequencing of the maize endospem ESTs
 Unpublished (2002)
 Contact: Lai, Jinsheng
 Dr. Joachim Messing's lab
 Waksman Institute, Rutgers University
 190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
 Tel: 732-445-3801
 Fax: 732-445-5735
 Email: jlai@waksman.rutgers.edu
 Seq primer: T3
 Location/Qualifiers
 1. .791
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="W22"
 /db_xref="taxon:4577"
 /tissue_type="Endospem_3"
 /clone_lib="Endospem_3"
 /note="vector: pbluescript SK-; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
 Query Match 17.8%; Score 461.8; DB 14; Length 791;
 Best Local Similarity 99.6%; Pred. No. 5.6e-109;
 Matches 463; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2134 TAGGAATCGTCACCTCGGCTGACAGCCCAAAAGGGATCCACCTGATCAGATCGGATTC 2193
 791 TAGGAATCGTCACCTCGGCTGACAGCCCAAAAGGGATCCACCTGATCAAGATCGGATTC 732
 2194 ACCGTACTCGAACGGAACGACAGGTGGTTTGGTTGGTTTGGTTGGTTTGGTTGGTT 2253
 731 ACCGTACTCGAACGGAACGACAGGTGGTTTGGTTGGTTTGGTTGGTTTGGTTGGTT 672
 2254 TCCAGCTGATTTTGTACCTCGGGAATACGCTCCAGGGGTAAACCATGGGCAAGTGA 2313
 671 TCCAGCTGATTTTGTACCTCGGGAATACGCTCCAGGGGTAAACCATGGGCAAGTGA 612
 2314 GGTCTTCTTGACCTACGACGAGCTCTCTCGCATCTGATATACGCTGGCTTGACCTCA 2373
 611 GGTCTTCTTGACCTACGACGAGCTCTCTCGCATCTGATATACGCTGGCTTGACCTCA 552
 2374 TTCTGGTCCCATATATTTAGGCTTGGGCTTAACCTCAGCTCGCTCGCATGGCGGTATG 2433
 551 TTCTGGTCCCATATATTTAGGCTTGGGCTTAACCTCAGCTCGCTCGCATGGCGGTATG 492
 2434 GAAACATCCCGATTGTCGCGAGACTGGAGGGCTCTTCGACACTGCTTTCGATGTGGACA 2493
 491 GGACCATCCCGATTGTCGCGAGACTGGAGGGCTCTTCGACACTGCTTTCGATGTGGACA 432

2494 ATGACAGGAACGAGCCGAGATCGAGGCTTGAAGCCCAACGCGTTTGTAGCTTTCACGAG 2553
 431 ATGACAGGAACGAGCCGAGATCGAGGCTTGAAGCCCAACGCGTTTGTAGCTTTCACGAG 372
 2554 CTGATAGCAACGCGTTTGTAGCTACGCGCTGACAGGCGGATCTCAG 2598
 371 CTGATAGCAACGCGTTTGTAGCTACGCGCTGACAGGCGGATCTCAG 327

RESULT 15
 CF038283/c
 LOCUS QCH1a11.yg QCH Zea mays cDNA clone QCH1a11, mRNA sequence. EST 17-JUL-2003
 DEFINITION CF038283
 ACCESSION CF038283.1 GI:32933471
 VERSION CF038283.1
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 466)
 Genoplante.
 Genoplante, a major partnership french program in plant genomics
 Unpublished (2003)
 Contact: Genoplante
 Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>)
 and <http://genoplante-info.inbio.gen.fr>.

FEATURES
 Location/Qualifiers
 1. .466
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="P2"
 /db_xref="taxon:4577"
 /clone="QCH1a11"
 /tissue_type="embryo"
 /clone_lib="QCH"

ORIGIN
 Query Match 17.7%; Score 459; DB 14; Length 466;
 Best Local Similarity 100.0%; Pred. No. 2.5e-108;
 Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1558 GGGGTGGTTCTGAAATAAATGTGTGGCTGGAGTGTGCGAGGCGCTTGTGTACTTCC 1617
 459 GGGGTGGTTCTGAAATAAATGTGTGGCTGGAGTGTGCGAGGCGCTTGTGTACTTCC 400
 1618 TGGAACTCAAAATGGATGTTTGGAGTCGGATATGATATGGCAGGAGCATGACCGCC 1677
 399 TGGAACTCAAAATGGATGTTTGGAGTCGGATATGATATGGCAGGAGCATGACCGCC 340
 1678 GATTGGCTTCTTCTGCTGCTTCTGCTCTAGAGTTTCTCTCCAAAGTGGATCTTCTCGA 1737
 339 GATTGGCTTCTTCTGCTGCTTCTGCTCTAGAGTTTCTCTCCAAAGTGGATCTTCTCGA 280
 1738 ACATAATACATGTCATGATTTGGTCAAGTGTCTCTGCTTGGCTGCTACACAGGAAACT 1797
 279 ACATAATACATGTCATGATTTGGTCAAGTGTCTCTGCTTGGCTGCTACACAGGAAACT 220
 1798 ACGGAAGTCTAGCTTGGCAAAACGACGGGTGATTCACCATCCAAATCTTGAATTTG 1857
 219 ACGGAAGTCTAGCTTGGCAAAACGACGGGTGATTCACCATCCAAATCTTGAATTTG 160
 1858 GAGCGCATCATTTGGCAAAACGATAGATATTTGTGATAAAGCAACACTGCTCTAATA 1917
 159 GAGCGCATCATTTGGCAAAACGATAGATATTTGTGATAAAGCAACACTGCTCTAATA 100

